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gctaattcca acgtgatagc tacagctgga gcattgggat accgggcacc tgagctctca 2220

aagctcaaga aagcaaacac taaaactgat atctacagtc ttggtgttat cttgttagaa 2280

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ccttctccat cagcacgacc agaagttcat caagttctcc agcagctgga agagattaga 2520

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Gln Cys Asp Ser Ser Ser His Val Thr Ser Ile Ser Leu Ala Ser His
         30                  35                  40

tcc ctc acc gga aca ctc ccc tcg gat ctc aat tcc ctc tct caa ctc      255
Ser Leu Thr Gly Thr Leu Pro Ser Asp Leu Asn Ser Leu Ser Gln Leu
     45                  50                  55

cgc act ctc tcc ctc caa gac aat tcc ctc acc ggc acc ctc cct tct      303
Arg Thr Leu Ser Leu Gln Asp Asn Ser Leu Thr Gly Thr Leu Pro Ser
60                  65                  70                  75

ctc tcc aac ctt tct ttc ctc caa acc gtc tac tta aac cgc aac aac      351
Leu Ser Asn Leu Ser Phe Leu Gln Thr Val Tyr Leu Asn Arg Asn Asn
                 80                  85                  90

ttc tcc tcc gtg tcc ccc acc gct ttc gcc tcc cta acc tcc ctc caa      399
Phe Ser Ser Val Ser Pro Thr Ala Phe Ala Ser Leu Thr Ser Leu Gln
             95                 100                 105

acc ctc agc ctc ggc tcc aac cct gct ctc caa ccc tgg tcc ttc ccc      447
Thr Leu Ser Leu Gly Ser Asn Pro Ala Leu Gln Pro Trp Ser Phe Pro
         110                 115                 120

acc gac ctc act tcc tcc tct aac cta atc gac ctc gac ctc gcc acc      495
Thr Asp Leu Thr Ser Ser Ser Asn Leu Ile Asp Leu Asp Leu Ala Thr
     125                 130                 135

gta tcc ctc acc ggt ccc ttg ccg gac att ttc gac aaa ttc cct tcc      543
Val Ser Leu Thr Gly Pro Leu Pro Asp Ile Phe Asp Lys Phe Pro Ser
140                 145                 150                 155

ctt caa cac ctt cgc ctc tct tac aac aac ctc acc ggc aat tta ccc      591
Leu Gln His Leu Arg Leu Ser Tyr Asn Asn Leu Thr Gly Asn Leu Pro
                 160                 165                 170

tcc tct ttc tcc gcc gcc aac aat ctc gaa acg ctc tgg ctc aac aac      639
Ser Ser Phe Ser Ala Ala Asn Asn Leu Glu Thr Leu Trp Leu Asn Asn
             175                 180                 185

cag gcc gcc ggc ttg tcc ggt acc ctc ctc gtc ctc tcc aac atg tct      687
Gln Ala Ala Gly Leu Ser Gly Thr Leu Leu Val Leu Ser Asn Met Ser
         190                 195                 200

gca tta aac cag tcc tgg ctc aat aag aac cag ttc acc ggt tcc ata      735
Ala Leu Asn Gln Ser Trp Leu Asn Lys Asn Gln Phe Thr Gly Ser Ile
     205                 210                 215

ccg gat tta tcg caa tgc acg gct ttg tct gac ttg cag ctc agg gat      783
Pro Asp Leu Ser Gln Cys Thr Ala Leu Ser Asp Leu Gln Leu Arg Asp
220                 225                 230                 235

aac cag tta act ggt gtg gtt ccc gct tca ttg aca agt ctt cct agt      831
Asn Gln Leu Thr Gly Val Val Pro Ala Ser Leu Thr Ser Leu Pro Ser
                 240                 245                 250
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ttg aag aaa gtt tct ctg gat aat aat gag ctt cag ggg cct gtg ccc   879
Leu Lys Lys Val Ser Leu Asp Asn Asn Glu Leu Gln Gly Pro Val Pro
          255   260   265

gtg ttt ggg aaa ggt gtg aat gtt act ctc gat ggg att aat agt ttt   927
Val Phe Gly Lys Gly Val Asn Val Thr Leu Asp Gly Ile Asn Ser Phe
          270   275   280

tgt ctt gat act cct ggg aat tgt gat ccc agg gtg atg gtt ttg ctg   975
Cys Leu Asp Thr Pro Gly Asn Cys Asp Pro Arg Val Met Val Leu Leu
     285   290   295

cag att gcc gag gca ttc ggg tat cca att cgg ttg gca gag tcg tgg   1023
Gln Ile Ala Glu Ala Phe Gly Tyr Pro Ile Arg Leu Ala Glu Ser Trp
300   305   310   315

aag ggg aat gat ccg tgt gat ggt tgg aac tat gtt gtg tgt gct gcc   1071
Lys Gly Asn Asp Pro Cys Asp Gly Trp Asn Tyr Val Val Cys Ala Ala
               320   325   330

gga aag att att act gtc aat ttc gag aaa cag ggt ttg cag ggt acc   1119
Gly Lys Ile Ile Thr Val Asn Phe Glu Lys Gln Gly Leu Gln Gly Thr
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atc tcc cct gca ttt gcc aat ttg act gac ttg agg act ttg ttt ctc   1167
Ile Ser Pro Ala Phe Ala Asn Leu Thr Asp Leu Arg Thr Leu Phe Leu
          350   355   360

aat ggc aat aat ttg atc ggt tct ata cct gat agt ttg atc act ttg   1215
Asn Gly Asn Asn Leu Ile Gly Ser Ile Pro Asp Ser Leu Ile Thr Leu
365   370   375

cct cag ctt cag act ctt gat gtg tct gac aac aac ctc tct gga ttg   1263
Pro Gln Leu Gln Thr Leu Asp Val Ser Asp Asn Asn Leu Ser Gly Leu
380   385   390   395

gtt cct aag ttc cca cca aag gtg aag ttg gtg act gcg gga aat gct   1311
Val Pro Lys Phe Pro Pro Lys Val Lys Leu Val Thr Ala Gly Asn Ala
               400   405   410

ttg ctt ggg aaa ccc ctt agt cct gga ggt gga cca agt gga act act   1359
Leu Leu Gly Lys Pro Leu Ser Pro Gly Gly Gly Pro Ser Gly Thr Thr
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cct tct ggg tct tcg acc ggt gga agt ggt ggt gaa tcc tca aag ggt   1407
Pro Ser Gly Ser Ser Thr Gly Gly Ser Gly Gly Glu Ser Ser Lys Gly
          430   435   440

aat tct tcg gtg tcg cca ggt tgg att gct ggt ata gtt gtt att gtg   1455
Asn Ser Ser Val Ser Pro Gly Trp Ile Ala Gly Ile Val Val Ile Val
     445   450   455

ttg ttt ttt att gca gtg gtg ttg ttt gtg tct tgg aag tgt ttt gtc   1503
Leu Phe Phe Ile Ala Val Val Leu Phe Val Ser Trp Lys Cys Phe Val
460   465   470   475

aac aag ctg cag ggg aag ttc agt agg gtt aaa ggt cat gaa aat ggg   1551

881

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Asn Lys Leu Gln Gly Lys Phe Ser Arg Val Lys Gly His Glu Asn Gly
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aaa gga ggc ttt aaa ctt gat gct gtc cat gtt tct aat gga tat ggt   1599
Lys Gly Gly Phe Lys Leu Asp Ala Val His Val Ser Asn Gly Tyr Gly
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ggt gtt cca gtt gag ttg caa agc cag agc agt ggt gat cga agt gac   1647
Gly Val Pro Val Glu Leu Gln Ser Gln Ser Ser Gly Asp Arg Ser Asp
            510                 515                 520

ctt cat gct tta gat ggt cca aca ttt tct atc caa gtt ctt cga caa   1695
Leu His Ala Leu Asp Gly Pro Thr Phe Ser Ile Gln Val Leu Arg Gln
        525                 530                 535

gtg acg aat aat ttc agc gag gag aac att tta ggc agg gga ggg ttt   1743
Val Thr Asn Asn Phe Ser Glu Glu Asn Ile Leu Gly Arg Gly Gly Phe
540                 545                 550                 555

gga gta gtt tat aag ggg gtg ttg cat gat gga aca aaa att gct gtt   1791
Gly Val Val Tyr Lys Gly Val Leu His Asp Gly Thr Lys Ile Ala Val
                560                 565                 570

aag agg atg gaa tct gtt gca atg ggg aac aaa ggt cag aaa gag ttc   1839
Lys Arg Met Glu Ser Val Ala Met Gly Asn Lys Gly Gln Lys Glu Phe
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gaa gca gag att gca ctt ctt agt aaa gtt agg cat aga cat ttg gtt   1887
Glu Ala Glu Ile Ala Leu Leu Ser Lys Val Arg His Arg His Leu Val
                590                 595                 600

gct ctt cta ggg tat tgc atc aat ggc aat gaa agg ctt ttg gtg tat   1935
Ala Leu Leu Gly Tyr Cys Ile Asn Gly Asn Glu Arg Leu Leu Val Tyr
        605                 610                 615

gag tat atg cct caa ggt aca tta aca cag cac ctg ttt gag tgg cag   1983
Glu Tyr Met Pro Gln Gly Thr Leu Thr Gln His Leu Phe Glu Trp Gln
620                 625                 630                 635

gag cat ggg tat gct cct ttg act tgg aag caa agg gta gta ata gct   2031
Glu His Gly Tyr Ala Pro Leu Thr Trp Lys Gln Arg Val Val Ile Ala
                640                 645                 650

ttg gat gta gcg cgg ggg gtg gaa tac ttg cac agt tta gct cag caa   2079
Leu Asp Val Ala Arg Gly Val Glu Tyr Leu His Ser Leu Ala Gln Gln
            655                 660                 665

agc ttc att cat aga gac tta aaa ccc tca aac ata cta cta ggc gat   2127
Ser Phe Ile His Arg Asp Leu Lys Pro Ser Asn Ile Leu Leu Gly Asp
        670                 675                 680

gac atg aga gca aag gtt gct gat ttt ggg ttg gtt aaa aat gca cca   2175
Asp Met Arg Ala Lys Val Ala Asp Phe Gly Leu Val Lys Asn Ala Pro
        685                 690                 695

gat ggg aag tat tct gtt gag aca cgg ttg gct gga aca ttt gga tat   2223
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ttggttatta cttcaatatc atgcttcggt gttcagcaaa tttaagtagt tcaccagagt   2392

aatcgctcac atacaaaaaa aaagtagaaa gagttgaagg gaaaataatt gatactcaat   2452

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gctcttttca cgtgtttgt tgagttgggt gggggtttg ctgcatagtt cttggtggtt     2572

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catgggctta ggtggtagtt ctctgtcgca actaatcact gttgtggaat ttatcattct   2752

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tcggtgttgt ttttatccat ttagcatcaa gactttgca agcataaaac ttcctaaaat    2872

gttgcattga atgtgattga atggcatttg attagtgcta gtctatttgt ttgattatat   2932

ttaatgttac tctgtttctt accag  ct act gga aga gtg aca acc aaa gtg      2983
                           Ala Thr Gly Arg Val Thr Thr Lys Val
                                           725                730

gat gtt tat gca ttt gga gta gtt ctg atg gaa ctt atc acc ggt aga    3031
Asp Val Tyr Ala Phe Gly Val Val Leu Met Glu Leu Ile Thr Gly Arg
                735                 740                 745

aag gca ttg gat gat act gtg cca gat gaa agg tct cac ttg gtg aca    3079
Lys Ala Leu Asp Asp Thr Val Pro Asp Glu Arg Ser His Leu Val Thr
                750                 755                 760

tgg ttc cgt agg gta cta att aac aag gaa aac att cca aag gca att    3127
Trp Phe Arg Arg Val Leu Ile Asn Lys Glu Asn Ile Pro Lys Ala Ile
            765                 770                 775

gat caa att ctc aat cca gat gag gaa acc atg gga agc ata tat aca    3175
Asp Gln Ile Leu Asn Pro Asp Glu Glu Thr Met Gly Ser Ile Tyr Thr
        780                 785                 790

gtg gcc gag ctg gca ggc cat tgc act gct cgc gaa cca tac caa agg    3223
Val Ala Glu Leu Ala Gly His Cys Thr Ala Arg Glu Pro Tyr Gln Arg
795                 800                 805                 810

ccg gat atg ggt cat gca gtg aac gtc ttg gtt cct ctt gtg gag caa    3271
Pro Asp Met Gly His Ala Val Asn Val Leu Val Pro Leu Val Glu Gln
                815                 820                 825

tgg aaa cct act agc cat gat gaa gaa gag gaa gac ggc tct ggc ggt    3319
Trp Lys Pro Thr Ser His Asp Glu Glu Glu Glu Asp Gly Ser Gly Gly
                830                 835                 840
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883

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gac ctt cat atg agc ctt cct caa gct cta cga agg tgg caa gcc aac        3367
Asp Leu His Met Ser Leu Pro Gln Ala Leu Arg Arg Trp Gln Ala Asn
        845                   850                   855


gaa ggc act tcc tca ata ttt aat gac att tcc atc tca caa acc caa        3415
Glu Gly Thr Ser Ser Ile Phe Asn Asp Ile Ser Ile Ser Gln Thr Gln
    860                   865                   870


tca agc atc tcc tct aaa cct gca ggg ttt gca gac tcc ttt gat tca        3463
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                     Met Ser Asn Phe Leu Lys Ser Leu Thr Pro Pro
                     1               5                   10


ccc tcg ggc tgg tct gaa aca acc cca ttc tgc caa tgg aag ggt atc        159
Pro Ser Gly Trp Ser Glu Thr Thr Pro Phe Cys Gln Trp Lys Gly Ile
            15                  20                  25


caa tgc gat tca tcc agc cac gtg acc agc ata agc ctc gct tcg cat        207
Gln Cys Asp Ser Ser Ser His Val Thr Ser Ile Ser Leu Ala Ser His
        30                  35                  40


tcc ctc acc gga aca ctc ccc tcg gat ctc aat tcc ctc tct caa ctc        255
Ser Leu Thr Gly Thr Leu Pro Ser Asp Leu Asn Ser Leu Ser Gln Leu
    45                  50                  55


cgc act ctc tcc ctc caa gac aat tcc ctc acc ggc acc ctc cct tct        303
Arg Thr Leu Ser Leu Gln Asp Asn Ser Leu Thr Gly Thr Leu Pro Ser
60                  65                  70                  75


ctc tcc aac ctt tct ttc ctc caa acc gtc tac tta aac cgc aac aac        351
Leu Ser Asn Leu Ser Phe Leu Gln Thr Val Tyr Leu Asn Arg Asn Asn
                80                  85                  90


ttc tcc tcc gtg tcc ccc acc gct ttc gcc tcc cta acc tcc ctc caa        399
Phe Ser Ser Val Ser Pro Thr Ala Phe Ala Ser Leu Thr Ser Leu Gln
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                    95                    100                   105

acc ctc agc ctc ggc tcc aac cct gct ctc caa ccc tgg tcc ttc ccc      447
Thr Leu Ser Leu Gly Ser Asn Pro Ala Leu Gln Pro Trp Ser Phe Pro
            110                   115                   120

acc gac ctc act tcc tcc tct aac cta atc gac ctc gac ctc gcc acc      495
Thr Asp Leu Thr Ser Ser Ser Asn Leu Ile Asp Leu Asp Leu Ala Thr
    125                   130                   135

gta tcc ctc acc ggt ccc ttg ccg gac att ttc gac aaa ttc cct tcc     543
Val Ser Leu Thr Gly Pro Leu Pro Asp Ile Phe Asp Lys Phe Pro Ser
140                   145                   150                   155

ctt caa cac ctt cgc ctc tct tac aac aac ctc acc ggc aat tta ccc     591
Leu Gln His Leu Arg Leu Ser Tyr Asn Asn Leu Thr Gly Asn Leu Pro
                160                   165                   170

tcc tct ttc tcc gcc gcc aac aat ctc gaa acg ctc tgg ctc aac aac     639
Ser Ser Phe Ser Ala Ala Asn Asn Leu Glu Thr Leu Trp Leu Asn Asn
                175                   180                   185

cag gcc gcc ggc ttg tcc ggt acc ctc ctc gtc ctc tcc aac atg tct     687
Gln Ala Ala Gly Leu Ser Gly Thr Leu Leu Val Leu Ser Asn Met Ser
        190                   195                   200

gca tta aac cag tcc tgg ctc aat aag aac cag ttc acc ggt tcc ata     735
Ala Leu Asn Gln Ser Trp Leu Asn Lys Asn Gln Phe Thr Gly Ser Ile
    205                   210                   215

ccg gat tta tcg caa tgc acg gct ttg tct gac ttg cag ctc agg gat     783
Pro Asp Leu Ser Gln Cys Thr Ala Leu Ser Asp Leu Gln Leu Arg Asp
220                   225                   230                   235

aac cag tta act ggt gtg gtt ccc gct tca ttg aca agt ctt cct agt     831
Asn Gln Leu Thr Gly Val Val Pro Ala Ser Leu Thr Ser Leu Pro Ser
                240                   245                   250

ttg aag aaa gtt tct ctg gat aat aat gag ctt cag ggg cct gtg ccc     879
Leu Lys Lys Val Ser Leu Asp Asn Asn Glu Leu Gln Gly Pro Val Pro
                255                   260                   265

gtg ttt ggg aaa ggt gtg aat gtt act ctc gat ggg att aat agt ttt     927
Val Phe Gly Lys Gly Val Asn Val Thr Leu Asp Gly Ile Asn Ser Phe
        270                   275                   280

tgt ctt gat act cct ggg aat tgt gat ccc agg gtg atg gtt ttg ctg     975
Cys Leu Asp Thr Pro Gly Asn Cys Asp Pro Arg Val Met Val Leu Leu
    285                   290                   295

cag att gcc gag gca ttc ggg tat cca att cgg ttg gca gag tcg tgg    1023
Gln Ile Ala Glu Ala Phe Gly Tyr Pro Ile Arg Leu Ala Glu Ser Trp
300                   305                   310                   315

aag ggg aat gat ccg tgt gat ggt tgg aac tat gtt gtg tgt gct gcc    1071
Lys Gly Asn Asp Pro Cys Asp Gly Trp Asn Tyr Val Val Cys Ala Ala
                320                   325                   330
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885

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gga aag att att act gtc aat ttc gag aaa cag ggt ttg cag ggt acc     1119
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atc tcc cct gca ttt gcc aat ttg act gac ttg agg act ttg ttt ctc     1167
Ile Ser Pro Ala Phe Ala Asn Leu Thr Asp Leu Arg Thr Leu Phe Leu
            350                 355                 360

aat ggc aat aat ttg atc ggt tct ata cct gat agt ttg atc act ttg     1215
Asn Gly Asn Asn Leu Ile Gly Ser Ile Pro Asp Ser Leu Ile Thr Leu
        365                 370                 375

cct cag ctt cag act ctt gat gtg tct gac aac aac ctc tct gga ttg     1263
Pro Gln Leu Gln Thr Leu Asp Val Ser Asp Asn Asn Leu Ser Gly Leu
380                 385                 390                 395

gtt cct aag ttc cca cca aag gtg aag ttg gtg act gcg gga aat gct     1311
Val Pro Lys Phe Pro Pro Lys Val Lys Leu Val Thr Ala Gly Asn Ala
                400                 405                 410

ttg ctt ggg aaa ccc ctt agt cct gga ggt gga cca agt gga act act     1359
Leu Leu Gly Lys Pro Leu Ser Pro Gly Gly Gly Pro Ser Gly Thr Thr
            415                 420                 425

cct tct ggg tct tcg acc ggt gga agt ggt ggt gaa tcc tca aag ggt     1407
Pro Ser Gly Ser Ser Thr Gly Gly Ser Gly Gly Glu Ser Ser Lys Gly
        430                 435                 440

aat tct tcg gtg tcg cca ggt tgg att gct ggt ata gtt gtt att gtg     1455
Asn Ser Ser Val Ser Pro Gly Trp Ile Ala Gly Ile Val Val Ile Val
        445                 450                 455

ttg ttt ttt att gca gtg gtg ttg ttt gtg tct tgg aag tgt ttt gtc     1503
Leu Phe Phe Ile Ala Val Val Leu Phe Val Ser Trp Lys Cys Phe Val
460                 465                 470                 475

aac aag ctg cag ggg aag ttc agt agg gtt aaa ggt cat gaa aat ggg     1551
Asn Lys Leu Gln Gly Lys Phe Ser Arg Val Lys Gly His Glu Asn Gly
                480                 485                 490

aaa gga ggc ttt aaa ctt gat gct gtc cat gtt tct aat gga tat ggt     1599
Lys Gly Gly Phe Lys Leu Asp Ala Val His Val Ser Asn Gly Tyr Gly
            495                 500                 505

ggt gtt cca gtt gag ttg caa agc cag agc agt ggt gat cgc agt gac     1647
Gly Val Pro Val Glu Leu Gln Ser Gln Ser Ser Gly Asp Arg Ser Asp
        510                 515                 520

ctt cat gct tta gat ggt cca aca ttt tct atc caa gtt ctt cga caa     1695
Leu His Ala Leu Asp Gly Pro Thr Phe Ser Ile Gln Val Leu Arg Gln
        525                 530                 535

gtg acg aat aat ttc agc gag gag aac att tta ggc agg gga ggg ttt     1743
Val Thr Asn Asn Phe Ser Glu Glu Asn Ile Leu Gly Arg Gly Gly Phe
540                 545                 550                 555

gga gta gtt tat aag ggg gtg ttg cat gat gga aca aaa att gct gtt     1791
Gly Val Val Tyr Lys Gly Val Leu His Asp Gly Thr Lys Ile Ala Val
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              560              565              570

aag agg atg gaa tct gtt gca atg ggg aac aaa ggt cag aaa gag ttc   1839
Lys Arg Met Glu Ser Val Ala Met Gly Asn Lys Gly Gln Lys Glu Phe
             575              580              585

gaa gca gag att gca ctt ctt agt aaa gtt agg cat aga cat ttg gtt   1887
Glu Ala Glu Ile Ala Leu Leu Ser Lys Val Arg His Arg His Leu Val
         590              595              600

gct ctt cta ggg tat tgc atc aat ggc aat gaa agg ctt ttg gtg tat   1935
Ala Leu Leu Gly Tyr Cys Ile Asn Gly Asn Glu Arg Leu Leu Val Tyr
     605              610              615

gag tat atg cct caa ggt aca tta aca cag cac ctg ttt gag tgg cag   1983
Glu Tyr Met Pro Gln Gly Thr Leu Thr Gln His Leu Phe Glu Trp Gln
620              625              630              635

gag cat ggg tat gct cct ttg act tgg aag caa agg gta gta ata gct   2031
Glu His Gly Tyr Ala Pro Leu Thr Trp Lys Gln Arg Val Val Ile Ala
             640              645              650

ttg gat gta gcg cgg ggg gtg gaa tac ttg cac agt tta gct cag caa   2079
Leu Asp Val Ala Arg Gly Val Glu Tyr Leu His Ser Leu Ala Gln Gln
         655              660              665

agc ttc att cat aga gac tta aaa ccc tca aac ata cta cta ggc gat   2127
Ser Phe Ile His Arg Asp Leu Lys Pro Ser Asn Ile Leu Leu Gly Asp
     670              675              680

gac atg aga gca aag gtt gct gat ttt ggg ttg gtt aaa aat gca cca   2175
Asp Met Arg Ala Lys Val Ala Asp Phe Gly Leu Val Lys Asn Ala Pro
     685              690              695

gat ggg aag tat tct gtt gag aca cgg ttg gct gga aca ttt gga tat   2223
Asp Gly Lys Tyr Ser Val Glu Thr Arg Leu Ala Gly Thr Phe Gly Tyr
700              705              710              715

ctt gca cct gag tat gca g gtacagaaag cctttgattt tagtttgta    2272
Leu Ala Pro Glu Tyr Ala
             720

caattgtgcc ttaattttga agttcatatt ttatatgctc gtatttggtg gttatagctg   2332

ttggttatta cttcaatatc atgcttcggt gttcagcaaa tttaagtagt tcaccagagt   2392

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gttgcattga atgtgattga atggcatttg attagtgcta gtcatttgt ttgattatat 2932

ttaatgttac tctgtttctt accag ct act gga aga gtg aca acc aaa gtg 2983
                        Ala Thr Gly Arg Val Thr Thr Lys Val
                                                725                 730

gat gtt tat gca ttt gga gta gtt ctg atg gaa ctt atc acc ggt aga 3031
Asp Val Tyr Ala Phe Gly Val Val Leu Met Glu Leu Ile Thr Gly Arg
                735                 740                 745

aag gca ttg gat gat act gtg cca gat gaa agg tct cac ttg gtg aca 3079
Lys Ala Leu Asp Asp Thr Val Pro Asp Glu Arg Ser His Leu Val Thr
            750                 755                 760

tgg ttc cgt agg gta cta att aac aag gaa aac att cca aag gca att 3127
Trp Phe Arg Arg Val Leu Ile Asn Lys Glu Asn Ile Pro Lys Ala Ile
        765                 770                 775

gat caa att ctc aat cca gat gag gaa acc atg gga agc ata tat aca 3175
Asp Gln Ile Leu Asn Pro Asp Glu Glu Thr Met Gly Ser Ile Tyr Thr
    780                 785                 790

gtg gcc gag ctg gca ggc cat tgc act gct cgc gaa cca tac caa agg 3223
Val Ala Glu Leu Ala Gly His Cys Thr Ala Arg Glu Pro Tyr Gln Arg
795                 800                 805                 810

ccg gat atg ggt cat gca gtg aac gtc ttg gtt cct ctt gtg gag caa 3271
Pro Asp Met Gly His Ala Val Asn Val Leu Val Pro Leu Val Glu Gln
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tgg aaa cct act agc cat gat gaa gaa gag gaa gac ggc tct ggc ggt 3319
Trp Lys Pro Thr Ser His Asp Glu Glu Glu Glu Asp Gly Ser Gly Gly
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gac ctt cat atg agc ctt cct caa gct cta cga agg tgg caa gcc aac 3367
Asp Leu His Met Ser Leu Pro Gln Ala Leu Arg Arg Trp Gln Ala Asn
        845                 850                 855

gaa ggc act tcc tca ata ttt aat gac att tcc atc tca caa acc caa 3415
Glu Gly Thr Ser Ser Ile Phe Asn Asp Ile Ser Ile Ser Gln Thr Gln
    860                 865                 870

tca agc atc tcc tct aaa cct gca ggg ttt gca gac tcc ttt gat tca 3463
Ser Ser Ile Ser Ser Lys Pro Ala Gly Phe Ala Asp Ser Phe Asp Ser
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                    Met Ser Asn Phe Leu Lys Ser Leu Thr Pro Pro
                    1               5                   10

ccc tcg ggc tgg tct gaa aca acc cca ttc tgc caa tgg aag ggt atc      159
Pro Ser Gly Trp Ser Glu Thr Thr Pro Phe Cys Gln Trp Lys Gly Ile
            15                  20                  25

caa tgc gat tca tcc agc cac gtg acc agc ata agc ctc gct tcg cag      207
Gln Cys Asp Ser Ser Ser His Val Thr Ser Ile Ser Leu Ala Ser Gln
        30                  35                  40

tcc ctc acc gga aca ctc ccc tcg gat ctc aat tcc ctc tct caa ctc      255
Ser Leu Thr Gly Thr Leu Pro Ser Asp Leu Asn Ser Leu Ser Gln Leu
    45                  50                  55

cgc act ctc tcc ctc caa gac aat tcc ctc acc ggc acc ctc cct tct      303
Arg Thr Leu Ser Leu Gln Asp Asn Ser Leu Thr Gly Thr Leu Pro Ser
60                  65                  70                  75

ctc tcc aac ctt tct ttc ctc caa acc gtc tac tta aac cgc aac aac      351
Leu Ser Asn Leu Ser Phe Leu Gln Thr Val Tyr Leu Asn Arg Asn Asn
                80                  85                  90

ttc tcc tcc gtg tcc ccc acc gct ttc gcc tcc cta acc tcc ctc caa      399
Phe Ser Ser Val Ser Pro Thr Ala Phe Ala Ser Leu Thr Ser Leu Gln
                95                  100                 105

acc ctc agc ctc ggc tcc aac cct gct ctc caa ccc tgg tcc ttc ccc      447
Thr Leu Ser Leu Gly Ser Asn Pro Ala Leu Gln Pro Trp Ser Phe Pro
            110                 115                 120

acc gac ctc act tcc tcc tct aac cta atc gac ctc gac ctc gcc acc      495
Thr Asp Leu Thr Ser Ser Ser Asn Leu Ile Asp Leu Asp Leu Ala Thr
    125                 130                 135

gta tcc ctc acc ggt ccc ttg ccg gac att ttc gac aaa ttc cct tcc      543
Val Ser Leu Thr Gly Pro Leu Pro Asp Ile Phe Asp Lys Phe Pro Ser
140                 145                 150                 155

ctt caa cac ctt cgc ctc tct tac aac aac ctc acc ggc aat tta ccc      591
Leu Gln His Leu Arg Leu Ser Tyr Asn Asn Leu Thr Gly Asn Leu Pro
                160                 165                 170

tcc tct ttc tcc gcc gcc aac aat ctc gaa acg ctc tgg ctc aac aac      639
Ser Ser Phe Ser Ala Ala Asn Asn Leu Glu Thr Leu Trp Leu Asn Asn
            175                 180                 185
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cag gcc gcc ggc ttg tcc ggt acc ctc ctc gtc ctc tcc aac atg tct    687
Gln Ala Ala Gly Leu Ser Gly Thr Leu Leu Val Leu Ser Asn Met Ser
        190                 195                 200

gca tta aac cag tcc tgg ctc aat aag aac cag ttc acc ggt tcc ata    735
Ala Leu Asn Gln Ser Trp Leu Asn Lys Asn Gln Phe Thr Gly Ser Ile
    205                 210                 215

ccg gat tta tcg caa tgc acg gct ttg tct gac ttg cag ctc agg gat    783
Pro Asp Leu Ser Gln Cys Thr Ala Leu Ser Asp Leu Gln Leu Arg Asp
220                 225                 230                 235

aac cag tta act ggt gtg gtt ccc gct tca ttg aca agt ctt cct agt    831
Asn Gln Leu Thr Gly Val Val Pro Ala Ser Leu Thr Ser Leu Pro Ser
                240                 245                 250

ttg aag aaa gtt tct ctg gat aat aat gag ctt cag ggg cct gtg ccc    879
Leu Lys Lys Val Ser Leu Asp Asn Asn Glu Leu Gln Gly Pro Val Pro
            255                 260                 265

gtg ttt ggg aaa ggt gtg aat gtt act ctc gat ggg att aat agt ttt    927
Val Phe Gly Lys Gly Val Asn Val Thr Leu Asp Gly Ile Asn Ser Phe
        270                 275                 280

tgt ctt gat act cct ggg aat tgt gat ccc agg gtg atg gtt ttg ctg    975
Cys Leu Asp Thr Pro Gly Asn Cys Asp Pro Arg Val Met Val Leu Leu
        285                 290                 295

cag att gcc gag gca ttc ggg tat cca att cgg ttg gca gag tcg tgg   1023
Gln Ile Ala Glu Ala Phe Gly Tyr Pro Ile Arg Leu Ala Glu Ser Trp
300                 305                 310                 315

aag ggg aat gat ccg tgt gat ggt tgg aac tat gtt gtg tgt gct gcc   1071
Lys Gly Asn Asp Pro Cys Asp Gly Trp Asn Tyr Val Val Cys Ala Ala
                320                 325                 330

gga aag att att act gtc aat ttc gag aaa cag ggt ttg cag ggt acc   1119
Gly Lys Ile Ile Thr Val Asn Phe Glu Lys Gln Gly Leu Gln Gly Thr
            335                 340                 345

atc tcc cct gca ttt gcc aat ttg act gac ttg agg act ttg ttt ctc   1167
Ile Ser Pro Ala Phe Ala Asn Leu Thr Asp Leu Arg Thr Leu Phe Leu
        350                 355                 360

aat ggc aat aat ttg atc ggt tct ata cct gat agt ttg atc act ttg   1215
Asn Gly Asn Asn Leu Ile Gly Ser Ile Pro Asp Ser Leu Ile Thr Leu
        365                 370                 375

cct cag ctt cag act ctt gat gtg tct gac aac aac ctc tct gga ttg   1263
Pro Gln Leu Gln Thr Leu Asp Val Ser Asp Asn Asn Leu Ser Gly Leu
380                 385                 390                 395

gtt cct aag ttc cca cca aag gtg aag ttg gtg act gcg gga aat gct   1311
Val Pro Lys Phe Pro Pro Lys Val Lys Leu Val Thr Ala Gly Asn Ala
                400                 405                 410

ttg ctt ggg aaa ccc ctt agt cct gga ggt gga cca agt gga act act   1359
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Leu Leu Gly Lys Pro Leu Ser Pro Gly Gly Gly Pro Ser Gly Thr Thr
            415                 420                 425

cct tct ggg tct tcg acc ggt gga agt ggt ggt gaa tcc tca aag ggt    1407
Pro Ser Gly Ser Ser Thr Gly Gly Ser Gly Gly Glu Ser Ser Lys Gly
        430                 435                 440

aat tct tcg gtg tcg cca ggt tgg att gct ggt ata gtt gtt att gtg    1455
Asn Ser Ser Val Ser Pro Gly Trp Ile Ala Gly Ile Val Val Ile Val
        445                 450                 455

ttg ttt ttt att gca gtg gtg ttg ttt gtg tct tgg aag tgt ttt gtc    1503
Leu Phe Phe Ile Ala Val Val Leu Phe Val Ser Trp Lys Cys Phe Val
460                 465                 470                 475

aac aag ctg cag ggg aag ttc agt agg gtt aaa ggt cat gaa aat ggg    1551
Asn Lys Leu Gln Gly Lys Phe Ser Arg Val Lys Gly His Glu Asn Gly
                480                 485                 490

aaa gga ggc ttt aaa ctt gat gct gtc cat gtt tct aat gga tat ggt    1599
Lys Gly Gly Phe Lys Leu Asp Ala Val His Val Ser Asn Gly Tyr Gly
            495                 500                 505

ggt gtt cca gtt gag ttg caa agc cag agc agt ggt gat cgc agt gac    1647
Gly Val Pro Val Glu Leu Gln Ser Gln Ser Ser Gly Asp Arg Ser Asp
            510                 515                 520

ctt cat gct tta gat ggt cca aca ttt tct atc caa gtt ctt cga caa    1695
Leu His Ala Leu Asp Gly Pro Thr Phe Ser Ile Gln Val Leu Arg Gln
        525                 530                 535

gtg acg aat aat ttc agc gag gag aac att tta ggc agg gga ggg ttt    1743
Val Thr Asn Asn Phe Ser Glu Glu Asn Ile Leu Gly Arg Gly Gly Phe
540                 545                 550                 555

gga gta gtt tat aag ggg gtg ttg cat gat gga aca aaa att gct gtt    1791
Gly Val Val Tyr Lys Gly Val Leu His Asp Gly Thr Lys Ile Ala Val
                560                 565                 570

aag agg atg gaa tct gtt gca atg ggg aac aaa ggt cag aaa gag ttc    1839
Lys Arg Met Glu Ser Val Ala Met Gly Asn Lys Gly Gln Lys Glu Phe
                575                 580                 585

gaa gca gag att gca ctt ctt agt aaa gtt agg cat aga cat ttg gtt    1887
Glu Ala Glu Ile Ala Leu Leu Ser Lys Val Arg His Arg His Leu Val
        590                 595                 600

gct ctt cta ggg tat tgc atc aat ggc aat gaa agg ctt ttg gtg tat    1935
Ala Leu Leu Gly Tyr Cys Ile Asn Gly Asn Glu Arg Leu Leu Val Tyr
        605                 610                 615

gag tat atg cct caa ggt aca tta aca cag cac ctg ttt gag tgg cag    1983
Glu Tyr Met Pro Gln Gly Thr Leu Thr Gln His Leu Phe Glu Trp Gln
620                 625                 630                 635

gag cat ggg tat gct cct ttg act tgg aag caa agg gta gta ata gct    2031
Glu His Gly Tyr Ala Pro Leu Thr Trp Lys Gln Arg Val Val Ile Ala
                640                 645                 650
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ttg gat gta gcg cgg ggg gtg gaa tac ttg cac agt tta gct cag caa     2079
Leu Asp Val Ala Arg Gly Val Glu Tyr Leu His Ser Leu Ala Gln Gln
          655                 660                 665

agc ttc att cat aga gac tta aaa ccc tca aac ata cta cta ggc gat     2127
Ser Phe Ile His Arg Asp Leu Lys Pro Ser Asn Ile Leu Leu Gly Asp
          670                 675                 680

gac atg aga gca aag gtt gct gat ttt ggg ttg gtt aaa aat gca cca     2175
Asp Met Arg Ala Lys Val Ala Asp Phe Gly Leu Val Lys Asn Ala Pro
      685                 690                 695

gat ggg aag tat tct gtt gag aca cgg ttg gct gga aca ttt gga tat     2223
Asp Gly Lys Tyr Ser Val Glu Thr Arg Leu Ala Gly Thr Phe Gly Tyr
700                 705                 710                 715

ctt gca cct gag tat gca g gtacagaaag cctttgattt tagttttgta          2272
Leu Ala Pro Glu Tyr Ala
              720

caattgtgcc ttaattttga agttcatatt ttatatgctc gtatttggtg gttatagctg   2332

ttggttatta cttccaatatc atgcttcggt gttcagcaaa tttaagtagt tcaccagagt  2392

aatcgctcac atacaaaaaa aaagtagaaa gagttgaagg gaaaataatt gatactcaat   2452

tcctagatac atggctactt caaaattctt tgtggctatt tctttgcaat gttatatttt   2512

gctcttttca cgtgtttttgt tgagttgggt gggggtttttg ctgcatagtt cttggtggtt  2572

gatgcctcaa aagatatgtc gagccatttt tagacagttt accagagtct gactctcaat   2632

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catgggctta ggtggtagtt ctctgtcgca actaatcact gttgtggaat ttatcattct   2752

atcccatttc cttgttggat cggtgcattg aaacatcttt tgttaaaact gttattttga   2812

tcggtgttgt tttttatccat ttagcatcaa gacttttgca agcataaaac ttcctaaaat  2872

gttgcattga atgtgattag atggcaattg attagtgcta gtcatttgt ttgattatat    2932

ttaatgttac tctgtttctt accag  ct act gga aga gtg aca acc aaa gtg     2983
                             Ala Thr Gly Arg Val Thr Thr Lys Val
                                         725                 730

gat gtt tat gca ttt gga gta gtt ctg atg gaa ctt atc acc ggt aga     3031
Asp Val Tyr Ala Phe Gly Val Val Leu Met Glu Leu Ile Thr Gly Arg
              735                 740                 745

aag gca ttg gat gat act gtg cca gat gag agg tct cac ttg gtg aca     3079
Lys Ala Leu Asp Asp Thr Val Pro Asp Glu Arg Ser His Leu Val Thr
              750                 755                 760

tgg ttc cgt agg gta cta att aac aag gaa aac att cca aag gca att     3127
Trp Phe Arg Arg Val Leu Ile Asn Lys Glu Asn Ile Pro Lys Ala Ile
          765                 770                 775
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gat caa att ctc aat cca gat gag gaa acc atg gga agc ata tat aca    3175
Asp Gln Ile Leu Asn Pro Asp Glu Glu Thr Met Gly Ser Ile Tyr Thr
    780                 785                 790

gtg gcc gag ctg gca ggc cat tgc act gct cgc gaa cca tac caa agg    3223
Val Ala Glu Leu Ala Gly His Cys Thr Ala Arg Glu Pro Tyr Gln Arg
795                 800                 805                 810

ccg gat atg ggt cat gca gtg aac gtc ttg gtt cct ctt gtg gag caa    3271
Pro Asp Met Gly His Ala Val Asn Val Leu Val Pro Leu Val Glu Gln
                815                 820                 825

tgg aaa cct act agc cat gat gaa gaa gag gaa gac ggc tct ggc ggt    3319
Trp Lys Pro Thr Ser His Asp Glu Glu Glu Glu Asp Gly Ser Gly Gly
            830                 835                 840

gac ctt cat atg agc ctt cct caa gct cta cga agg tgg caa gcc aac    3367
Asp Leu His Met Ser Leu Pro Gln Ala Leu Arg Arg Trp Gln Ala Asn
        845                 850                 855

gaa ggc act tcc tca ata ttt aat gac att tcc atc tca caa acc caa    3415
Glu Gly Thr Ser Ser Ile Phe Asn Asp Ile Ser Ile Ser Gln Thr Gln
    860                 865                 870

tca agc atc tcc tct aaa cct gca ggg ttt gca gac tcc ttt gat tca    3463
Ser Ser Ile Ser Ser Lys Pro Ala Gly Phe Ala Asp Ser Phe Asp Ser
875                 880                 885                 890

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Met Asp Cys Arg


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                   Met Ser Asn Phe Leu Lys Ser Leu Thr Pro Pro
                   1               5                   10

ccc tcg ggc tgg tct gaa aca acc cca ttc tgc caa tgg aag ggt atc      159
Pro Ser Gly Trp Ser Glu Thr Thr Pro Phe Cys Gln Trp Lys Gly Ile
            15                  20                  25

caa tgc gat tca tcc agc cac gtg acc agc ata agc ctc gct tcg cag      207
Gln Cys Asp Ser Ser Ser His Val Thr Ser Ile Ser Leu Ala Ser Gln
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     45                    50                    55

cgc act ctc tcc ctc caa gac aat tcc ctc acc ggc acc ctc cct tct      303
Arg Thr Leu Ser Leu Gln Asp Asn Ser Leu Thr Gly Thr Leu Pro Ser
60                    65                    70                    75

ctc tcc aac ctt tct ttc ctc caa acc gtc tac ttc aac cgc aac aac      351
Leu Ser Asn Leu Ser Phe Leu Gln Thr Val Tyr Phe Asn Arg Asn Asn
                    80                    85                    90

ttc tcc tcc gtg tcc ccc acc gcc ttc gcc tcc cta acc tcc ctc caa      399
Phe Ser Ser Val Ser Pro Thr Ala Phe Ala Ser Leu Thr Ser Leu Gln
                 95                    100                   105

acc ctc agc ctc ggc tcc aac cct gct ctc caa ccc tgg tcc ttc ccc      447
Thr Leu Ser Leu Gly Ser Asn Pro Ala Leu Gln Pro Trp Ser Phe Pro
             110                   115                   120

acc gac ctc act tcc tcc tct aac cta atc gac ctc gac ctc gcc acc      495
Thr Asp Leu Thr Ser Ser Ser Asn Leu Ile Asp Leu Asp Leu Ala Thr
     125                   130                   135

gta tcc ctc acc ggt ccc ttg ccg gac att ttc gac aaa ttc cct tcc      543
Val Ser Leu Thr Gly Pro Leu Pro Asp Ile Phe Asp Lys Phe Pro Ser
140                   145                   150                   155

ctt caa cac ctt cgc ctc tct tac aac aac ctc acc ggc aat tta ccc      591
Leu Gln His Leu Arg Leu Ser Tyr Asn Asn Leu Thr Gly Asn Leu Pro
                 160                   165                   170

tcc tct ttc tcc gcc gcc aac aat ctc gaa acg ctc tgg ctc aac aac      639
Ser Ser Phe Ser Ala Ala Asn Asn Leu Glu Thr Leu Trp Leu Asn Asn
                 175                   180                   185

cag gcc gcc ggc ttg tcc ggt acc ctc ctc gtc ctc tcc aac atg tct      687
Gln Ala Ala Gly Leu Ser Gly Thr Leu Leu Val Leu Ser Asn Met Ser
             190                   195                   200

gca tta aac cag tcc tgg ctc aat aag aac cag ttc acc ggt tcc att      735
Ala Leu Asn Gln Ser Trp Leu Asn Lys Asn Gln Phe Thr Gly Ser Ile
     205                   210                   215

ccg gat tta tcg caa tgc acg gct ttg tct gac ttg cag ctc agg gat      783
Pro Asp Leu Ser Gln Cys Thr Ala Leu Ser Asp Leu Gln Leu Arg Asp
220                   225                   230                   235

aac cag tta act ggt gtg gtt ccc gct tca ttg aca agt ctt cct agt      831
Asn Gln Leu Thr Gly Val Val Pro Ala Ser Leu Thr Ser Leu Pro Ser
                 240                   245                   250

ttg aag aaa gtt tct ctg gat aat aat gag ctt cag ggg cct gtg ccc      879
Leu Lys Lys Val Ser Leu Asp Asn Asn Glu Leu Gln Gly Pro Val Pro
             255                   260                   265
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894

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gtg ttt ggg aaa ggt gtg aat gtt act ctc gat ggg att aat agt ttt      927
Val Phe Gly Lys Gly Val Asn Val Thr Leu Asp Gly Ile Asn Ser Phe
        270                 275                 280

tgt ctt gat act cct ggg aat tgt gat ccc agg gtg atg gtt ttg ctg      975
Cys Leu Asp Thr Pro Gly Asn Cys Asp Pro Arg Val Met Val Leu Leu
    285                 290                 295

cag att gcc gag gca ttc ggg tat cca att cgg ttg gca gag tcg tgg     1023
Gln Ile Ala Glu Ala Phe Gly Tyr Pro Ile Arg Leu Ala Glu Ser Trp
300                 305                 310                 315

aag ggg aat gat ccg tgt gat ggt tgg aac tat gtt gtg tgt gct gcc     1071
Lys Gly Asn Asp Pro Cys Asp Gly Trp Asn Tyr Val Val Cys Ala Ala
                320                 325                 330

gga aag att att act gtc aat ttc gag aaa cag ggt ttg cag ggt acc     1119
Gly Lys Ile Ile Thr Val Asn Phe Glu Lys Gln Gly Leu Gln Gly Thr
            335                 340                 345

atc tcc cct gca ttt gcc aat ttg act gac ttg agg act ttg ttt ctc     1167
Ile Ser Pro Ala Phe Ala Asn Leu Thr Asp Leu Arg Thr Leu Phe Leu
        350                 355                 360

aat ggc aat aat ttg atc ggt tct ata cct gat agt ttg atc act ttg     1215
Asn Gly Asn Asn Leu Ile Gly Ser Ile Pro Asp Ser Leu Ile Thr Leu
    365                 370                 375

cct cag ctt cag act ctt gat gtg tct gac aac aac ctc tct gga ttg     1263
Pro Gln Leu Gln Thr Leu Asp Val Ser Asp Asn Asn Leu Ser Gly Leu
380                 385                 390                 395

gtt cct aag ttc cca cca aag gtg aag ttg gtg act gcg gga aat gct     1311
Val Pro Lys Phe Pro Pro Lys Val Lys Leu Val Thr Ala Gly Asn Ala
                400                 405                 410

ttg ctt ggg aaa ccc ctt agt cct gga ggt gga cca agt gga act act     1359
Leu Leu Gly Lys Pro Leu Ser Pro Gly Gly Gly Pro Ser Gly Thr Thr
            415                 420                 425

cct tct ggg tct tcg acc ggt gga agt ggt ggt gaa tcc tca aag ggt     1407
Pro Ser Gly Ser Ser Thr Gly Gly Ser Gly Gly Glu Ser Ser Lys Gly
        430                 435                 440

aat tct tcg gtg tcg cca ggt tgg att gct ggt ata gtt gtt att gtg     1455
Asn Ser Ser Val Ser Pro Gly Trp Ile Ala Gly Ile Val Val Ile Val
    445                 450                 455

ttg ttt ttt att gca gtg gtg ttg ttt gtg tct tgg aag tgt ttt gtc     1503
Leu Phe Phe Ile Ala Val Val Leu Phe Val Ser Trp Lys Cys Phe Val
460                 465                 470                 475

aac aag ctg cag ggg aag ttc agt agg gtt aaa ggt cat gaa aat ggg     1551
Asn Lys Leu Gln Gly Lys Phe Ser Arg Val Lys Gly His Glu Asn Gly
                480                 485                 490

aaa gga ggc ttt aaa ctt gat gct gtc cat gtt tct aat gga tat ggt     1599
Lys Gly Gly Phe Lys Leu Asp Ala Val His Val Ser Asn Gly Tyr Gly
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              495              500              505

ggt gtt cca gtt gag ttg caa agc cag agc agt ggt gat cgc agt gac    1647
Gly Val Pro Val Glu Leu Gln Ser Gln Ser Ser Gly Asp Arg Ser Asp
        510              515              520

ctt cat gct tta gat ggt cca aca ttt tct atc caa gtt ctt cga caa    1695
Leu His Ala Leu Asp Gly Pro Thr Phe Ser Ile Gln Val Leu Arg Gln
    525              530              535

gtg acg aat aat ttc agc gag gag aac att tta ggc agg gga ggg ttt    1743
Val Thr Asn Asn Phe Ser Glu Glu Asn Ile Leu Gly Arg Gly Gly Phe
540              545              550              555

gga gta gtt tat aag ggg gtg ttg cat gat gga aca aaa att gct gtt    1791
Gly Val Val Tyr Lys Gly Val Leu His Asp Gly Thr Lys Ile Ala Val
              560              565              570

aag agg atg gaa tct gtt gca atg ggg aac aaa ggt cag aaa gag ttc    1839
Lys Arg Met Glu Ser Val Ala Met Gly Asn Lys Gly Gln Lys Glu Phe
        575              580              585

gaa gca gag att gca ctt ctt agt aaa gtt agg cat aga cat ttg gtt    1887
Glu Ala Glu Ile Ala Leu Leu Ser Lys Val Arg His Arg His Leu Val
    590              595              600

gct ctt cta ggg tat tgc atc aat ggc aat gaa agg ctt ttg gtg tat    1935
Ala Leu Leu Gly Tyr Cys Ile Asn Gly Asn Glu Arg Leu Leu Val Tyr
        605              610              615

gag tat atg cct caa ggt aca tta aca cag cac ctg ttt gag tgg cag    1983
Glu Tyr Met Pro Gln Gly Thr Leu Thr Gln His Leu Phe Glu Trp Gln
620              625              630              635

gag cat ggg tat gct cct ttg act tgg aag caa agg gta gta ata gct    2031
Glu His Gly Tyr Ala Pro Leu Thr Trp Lys Gln Arg Val Val Ile Ala
              640              645              650

ttg gat gta gcg cgg ggg gtg gaa tac ttg cac agt tta gct cag caa    2079
Leu Asp Val Ala Arg Gly Val Glu Tyr Leu His Ser Leu Ala Gln Gln
              655              660              665

agc ttc att cat aga gac tta aaa ccc tca aac ata cta cta ggc gat    2127
Ser Phe Ile His Arg Asp Leu Lys Pro Ser Asn Ile Leu Leu Gly Asp
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906

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<223>   Seq ID: 240017_region_G3__70509_14

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agacccatct tcgctgagga tgccgtgagg gaagttgcga atgggagaag agagggtgta  120

attgtagagc gtgtttccgt c                                             141


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atgagaggac ataaagggct aa                                            142


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agaaagaatg gacatgtgtc agctg                                         145
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<223>     Seq ID: 240017_region_G3__169084_14

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aaaaattcag aaggagcaac ctttgc                                        146
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<223>   Seq ID: 240O17_region_G3__94891_14

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acaatgcctt cttctcttca gttggaggtg ctgtagtgct tgaaacagtt gcatcgtttg   180

gccttatgtt cttcttcttc atatggtgtg ttaaaatgga tgttgccaca ttgatgaaga   240·

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<223>   Seq ID: 240O17_region_G3__281852_61

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aaacgacgga ggattaatga aagactg   147

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<223>   Seq ID: 240O17_region_G3__46583_12

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aaaaaccatt cttcaacttg caacaca   147

<210>   73
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<223>   Seq ID: 240O17_region_G3__306835_13

<400>   73

agtctcccag atgatcaatt ctgctcatag gcttttattg cttgcattct atgtccattt   60

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gaagcaaggg aaagcaaaga agctaatat                                     149
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<223>      Seq ID: 240017_region_G3__257208_12

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gcccatgtgc cagccagaat catagtaatt                                    150
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<223>      Seq ID: 240017_region_G3__150390_17

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gcttgcatgc atgcatgcat ttgtattaac tagggctgga tagctagctt aggcggcctc   120

tactatcatg gtgattaaac ttcacaccct                                    150
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<223>   Seq ID: 240017_region_G3__34697_75

<400>   77

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<223>   Seq ID: 240017_region_G3__150374_13

<400>   78

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tactatcatg gtgattaaac ttcacaccct   150

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<223>   Seq ID: 240017_region_G3__40513_22

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ttgcattcag gtgtggcttc acatttattt g   151

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<223>   Seq ID: 240017_region_G3__268602_14

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gcttcggcgc cgaagccaga ggagattccg ct                                 152


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<400>      82

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tatatatagc attcctctta acaaatctgt gc                                 152


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<223>      Seq ID: 240017_region_G3__139131_13

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gaggtaagaa aagggaaata tcattttctc attcatcccc ttgcttgtta tttacatgga   120

tatatatagc attcctctta acaaatctgt gc                                 152


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<223>      Seq ID: 240017_region_G3__203855_12

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tgatgctgca ggagattcct tctaaattag ctaactgaat accactaaca acaacaacga  120

gatgcctaaa acaacacaga tgtgagcaca tga                                153
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<223>      Seq ID: 240017_region_G3__199049_15

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ggtgcttcgt ttggttatgg tttatgaaat tatactaaca aaaaaaagtt tcacatcagt  120

taatttcatt tgctcagtga gtttatttgg tga                                153
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<223>      Seq ID: 240017_region_G3__320907_12

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ggggaacctt cgcggcggct cggataagtt gcagaggaaa atcggcgggc cgcgggggcg  120

gagagggcgg aggatggcga gcttaatatc ggag                               154
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<223>      Seq ID: 240017_region_G3__16407_17

<400>      87
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attttgctgg aaatcccacg tggatcagtg atat                               154
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<223>   Seq ID: 240O17_region_G3__206516_17

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ggcgattggc gtcggagctg gtcccaatcc gagt   154

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<223>   Seq ID: 240O17_region_G3__156785_13

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agaacagcgt cctctttctc tctcttcaac gccaac   156

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gtctcgccgc cgccgcctcc cgacttcaac ttccgccgcg aaatcgcgcg cctcgccgac   120

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tacaattata gtgatatgaa cttgcttcca caaccct   157


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aagtagcgaa gtggagttgc aaattgagct aaggaaa   157

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gtgcaataaa aattggttta ccttatcaga cttggga   157

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<223>   Seq ID: 240017_region_G3__29646_14

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aatacataac tatatcagtg gacgatgatc attattca   158

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gtggctattt ttctctgggt tatgaataag ggtttgga                          158


<210>      100
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tggttatgac ctgtgaatgt gatactactg acgatggg                          158


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918

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919

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920

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gcacaaaata tattttatta gccagaaagc actgacatta tgg                      163


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aacattaatg tctcaatcca tggacgttgg aggtaatacg cata                     164


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caaaaataaa taaataacct taacaatttc ccttctgtgc aatctc                   166
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tggcaggcga ggattccatg ggaagaaatg gaaatggaag aatgggag                 168
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atggaaaaca gagaaacaag aagaaaagac ggaacagcgt caaataaac   169

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<223>   Seq ID: 240O17_region_G3__55291_15

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ctcacagttt cacctaatga taaagagtgc caacattact gcaagaacag   170


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<223>    Seq ID: 240017_region_G3__303308_19

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925

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<400>      131

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aaaaaaatga atgtttttc ttcttttctt ttcttttttt cattagggtc atcgtacgag  180

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cta                                                                183


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tctctctcta taagttatat atttatatac aaaaagacga aattcgtaag gcaatcttat  180

tggt                                                               184


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<223>     Seq ID: 240017_region_G3__228643_13

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acctcttaac ttgcttcaaa atgaaacctc ttgcattaat ccaatcgtgc attgaatgag  180

tataa                                                       185


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tcattctgtt ggaaaaataa aataaaaatg aaggaaaata aatacgaaga agatgcacag  180

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tgaatagtgg ggaaaaaaat atttttttgca ataãataaat tactgtaggc agtgagaagg  180

caagaagat                                                          189


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cgtccaactc a                                                       191


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atttaaatt atgaaaatca atattgtatt attttgattt atgttgatga tttccaatgg  180

attagactgc tc                                                      192


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gaaattgtgg ttttctgttg tttaattttg cttttggaca aagattaaac ggttaaagtg   180

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tattatagtt ctgttttgta attaagttct ctttttcctt agttattgtg cttgtttaaa   180

atacatttgg tggcaagagc atagaa                                         206


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931

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gaaagtgata actaattttt ctctctaaga ctgttggaaa aataaaataa aaatgaagga  180

aaataaatac gaagaagatg cacagtcttg aat                               213


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<223>      Seq ID: 240017_region_G3__201115_11

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gatatatata tacataaaaa acaatatatt ttttgttcca tcattttgct tgcatgattt  180

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attttagtta aataaaataa acatttattt ttcaaattct acaagctaat aaactagtat   180

tactaaatgc atagagtatg agcaaattcg tgtaggtgga tt                      222


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tatatatata tatatatata tatatttgag tatggaagga gtactctatt caatgagatg   180

aatatgtgtt aacaaaaaga ttgattaggc gattaagaaa gaagaga                 227


<210>      153
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<223>      Seq ID: 240O17_region_G3__11301_29

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ttaactaaat caagcaaaaa caatggataa gatggaagtt tagtgataca aaaatatata   180

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<223>      Seq ID: 240017_region_G3__141875_12

<400>      154

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tttgtttttta attagaaaag catttaatta ttattatttt taacatattg ttaattgaaa  180

aaatatttt gccattggtc tgattttcta cactactcaa cacaacaatt tgctca        236


<210>      155
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<212>      DNA
<213>      Glycine max

<223>      Seq ID: 240017_region_G3__98090_18

<400>      155

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atatatatat aatattagtc atctttcaaa agtaaattat atatattgat taaccatttg  120

atattttctg agcgtggaaa tcggtgaaac ggtgggcagt ggcttttaca agttgctctt  180

ttttgtttata aaaatttgca agttgctctg aagcttctgc ggattgtact gcatatgt   238


<210>      156
<211>      244
<212>      DNA
<213>      Glycine max

<223>      Seq ID: 240017_region_G3__43298_35

<400>      156

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aaaaataatt catttatttt gaatacatga cttttatata tatatatata tatatatata  180

tatatatatc aaccgggaca tagtaattca agactactta atgttgttca cccgtgatac  240

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<223>      Seq ID: 240017_region_G3__262094_11

<400>      157

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attcaaaata ttttagttat ggaacaaaac tatatatata tatatgtgtg tgtgtgatta  120

tattacttttt ttaactaaat ttaaattata gagatgattt ataattatac atacaagtta  180

tgttatatga agaaaaaata aaaatttagg gggacaattg ccccttcatt cacaaagtgt  240

cattagaa                                                            248


<210>      158
<211>      248
<212>      DNA
<213>      Glycine max

<223>      Seq ID: 240017_region_G3__262079_15

<400>      158

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attcaaaata ttttagttat ggaacaaaac tatatatata tatatgtgtg tgtgtgatta  120

tattacttttt ttaactaaat ttaaattata gagatgattt ataattatac atacaagtta  180

tgttatatga agaaaaaata aaaatttagg gggacaattg ccccttcatt cacaaagtgt  240

cattagaa                                                            248


<210>      159
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<212>      DNA
<213>      Glycine max

<223>      Seq ID: 240017_region_G3__59090_12

<400>      159

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tcacaagcat aatgtaaaaa aaataatatt atttctcata accctatata tatatacacg  120

ccacataata cgtacgaacg taagtgatac tatcatgaaa gttcttgaat ggctttcttt  180

tcagggtgaa tacatatatt aatggatagt ggtttttgtt ggtcattgtt tcttattatt  240

atgtccttag gcacggtgtt agg                                          263


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<223>     Seq ID: 240017_region_G3__245723_13

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cctcttcttt ttattctttg aaaactacta aattcaaagc aaatcttaat tagaaagcaa   120

aaaagaaaga cataggttaa tgatattttt gctctctcaa ttttcacact aaactttta   180

gttccataat caatatctaa aaacacgatt aagaagaaga aaaataaata aatagcaagc   240

aaacaaacaa ttattatcca cgcgc                                         265


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<213>     Glycine max

<223>     Seq ID: 240017_region_G3__194628_54

<400>     161

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atatatatat atatatataa atatatatat atatatatat aattaattt tacaataatt   120

attttaaata ttatacgtat tacaatatct cattacttta cattgtaaaa catttttacaa   180

tgaaaaaact cctagattct ataaatattt tcttttagag ttacaatttt attacacggc   240

aactgacgtg tcggagttgg taacat                                        266


<210>     162
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<212>     DNA
<213>     Glycine max

<223>     Seq ID: 240017_region_G3__4566_16

<400>     162

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ctaattgaaa aataacaaaa caatacttat gaattatatg taagtgttgt cctaaactaa   120

actaaaccaa tcaacaaaga aaataatctca aattctaatt gaaacaaatg aaaagatcat   180

ttcactgttc tagataaatt ttatgatata taatgtaaaa gtgaattaat acctaaatta   240

agatagtaca caggcaaact tcaagaaa                                       268
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<223>      Seq ID: 240O17_region_G3__96209_14

<400>      163

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taacttgttg acccaacata ttatttaaga aaaataaaat aaaaaatatt tttattagaa  120

aggaaaaaat tatgttttg ttgattttt atacccttt aaaatttata taataaatat  180

ttttctcatt taattttta acatgtgcta agaacattta tgagtaatat ttttatttgt  240

catatttga agagggagcg aaagcctaca ttac                              274


<210>      164
<211>      274
<212>      DNA
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<223>      Seq ID: 240O17_region_G3__248715_17

<400>      164

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gaattaaata tcacagtgaa atttaaatta aattaaattg ataacatatg tatttatttt  120

ctaatttaaa aaaaactgtc aaaaaaaatt cttttttata taaggatgat gttaatttaa  180

tttatttttg agttgttaat cttaacaata cgagtagcta taatagacag cgatatcgag  240

ttgttaatac gagtagcaag caataccaca agaa                             274


<210>      165
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<212>      DNA
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<223>      Seq ID: 240O17_region_G3__71410_40

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taataataat aataataata ataataataa taaaagttta ggaagaaaaa tgagaaaact  120

aattagtttc gggttttatt taaggttttt ttagtttcag aaactaaaat gacatatatga  180

tacaaattta aagattaaat tcgtcattta ctcattttt attagacaaa atttaggttt  240

aagcatgcat acctttgtt tcttgaatct agccaaactt                        280
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<223>      Seq ID: 240017_region_G3__226519_13

<400>      166

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ccatatatct cacatttttt aggaggggaa ggataaggtt atatcacttt atttgtgtaa  180

gtaacttttt tggattaata attgattatt attattaaat aagacaaccc gaatataact  240

ttttcatttt tgagggagca tgaaagttgg agtacggaaa tgga                   284


<210>      167
<211>      285
<212>      DNA
<213>      Glycine max

<223>      Seq ID: 240017_region_G3__11282_19

<400>      167

cgaaattcgt aaggcaatct tattggtatt ataattttct ctactgatta tgtctaacca   60

tttatacaca cacacacaca cacatatata tatatatata tatatatata tattattact  120

tgttaaataa aatcagaaaa atgttgtaat cactttcaaa actgtagtta ataaacctta  180

actaaatcaa gcaaaaacaa tggataagat ggaagtttag tgatacaaaa atatatacag  240

gtatagtgag aataaaaaag ttgaggaagt gtgaaatcta cgtga                  285


<210>      168
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<212>      DNA
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<223>      Seq ID: 240017_region_G3__170504_12

<400>      168

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cttaattata ttgaacaaaa aataaatatta tatattaata ataataaata aatttccactt  120

aaaagtgtca ttaattataa attttttttta accaaagcga tatcgttttg ataagttaaa  180

aaaaaaacg gttaatacaa gttttttaact gatttaacga ttttaaatcg atgtaaggat  240
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ccattaattt ttaggagctc ccactggccc gatttggatt tcattt            286


<210>      169
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<223>      Seq ID: 240017_region_G3__40864_14

<400>      169

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ttccgtacat tataaataat attatatacg tcatatttac atcatttttt atccttgttt   180

atctcaaaaa agtgtaaata tagagagagt atatatcata tcatataata tgtaagtttt   240

tattagttta aaaaaatagc ttgagagtaa tgtgatttgt catgtgc                 287


<210>      170
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<213>      Glycine max

<223>      Seq ID: 240017_region_G3__13529_14

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attttttctt atttctctta aactagatac tatcgaatcc attctatttc ttatctgttt   120

ccattattct acttctcact tattttcatt actttattcc tttctttttat gtttctatcc   180

actttatttta tcacctattt ctttcttttct taccgaatac taaacaagcc ttgtgatccg   240

aaagcccgaa acaatcattt tttatgaaac agcttacact ctggtggtgt g            291


<210>      171
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<223>      Seq ID: 240017_region_G3__22858_14

<400>      171

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atttatgtaa agttatttta tttggttaca ataattaaaa aatgtacttt atattataaa   120

aagtagttat aattttgact tttttttcagc tgctactcaa agtagcttct gaaaataatc   180
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atatagatag atagattctg atttttttc taaaaaaaaa cttaaacaaa cacactaaga  240

aattttagaa gtgattttc atgaaaaaag ttgaaacaaa tgggctctaa a           291


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<223>      Seq ID: 240017_region_G3__309211_13

<400>      172

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atttatttat tttcattatt cctaaactaa ataactttgt ttcttattcta cttcttatat  180

atttctattc acctttttta atttctagtt atcatatctt gtacttcttt taatttttct  240

tccaaccaaa catatttaga aactactctt gggataatca gcagtagtgt tt          292


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<223>      Seq ID: 240017_region_G3__55568_26

<400>      173

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aacaaaaact aatgtagaaa tgatctagaa aactttttt ttaagttcta actcttttc  180

atcaatgtta tacatatata tatatatata tatatatatc ccaaaataac caatcaaata  240

aactacttag tttacttata tgttaaatca tcgacctatt acaagagagg agg         293


<210>      174
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<223>      Seq ID: 240017_region_G3__73238_16

<400>      174

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aaattaagat ttttttcta atttctagat atattaatta ttttttttctt aaatattctt  120
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acttaattat tttctcatca aatattaatg agatgaatag agaaataaga aaagaataat   180

ttttgaatga taatataatt aattaattaa taaatttaat gtgattaatt aaattaatta   240

tttttcttaa gacacataaa ttagttgaaa ggtaattgta ataagggaca gacggagtga   300
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<223>      Seq ID: 240O17_region_G3__52488_19

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atattgacat gttcttatat atatatatat atatgaggga ttgtattatc tctgaaaaaa   120

gatttttatca taaaatcata atgatttctc ataatgtatc tttacatttt aaagttagat   180

aaataaaatt gattttaaat tgttagatat aattaaaata cataattaat atgacttta   240

acaaattgat atataaacac ttaaaaaaaa gtttcatgac gtacggtgtg tattgttggt   300
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<223>      Seq ID: 318O13_region_A3__471518_14

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tttctttttt tcctattagg agaatctcgc gtaattacat aatt                    104
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<223>      Seq ID: 318O13_region_A3__231599_23

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tgctgaatcc gacagcgact ccgaggagga ggagtacgag gacct                   105
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<223>      Seq ID: 318O13_region_A3__375912_13

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ctgtcgcgaa gaagaagaag gcgtcgcgag gaagaagaag gcgtaggttt            110


<210>      179
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<223>      Seq ID: 318O13_region_A3__180013_12

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tagcggcggc ggcgtggtcc tgggtggaga agatgttgca ggagcaccag             110


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<223>      Seq ID: 318O13_region_A3__171606_14

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gagtttagtt tagttatcaa ttgcagggac ttcttcagtc ccacattgga aag          113


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<223>      Seq ID: 318O13_region_A3__416256_13

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<223>   Seq ID: 318O13_region_A3__231395_15

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tttctttctt tatttatcag cgattcgtgg caatttttcg aaggtagggt ttgatgggtg   120

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<223>   Seq ID: 318O13_region_A3__5502_47

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aaagc   125

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gcctc   125

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gcgtttgg                                                            128


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<223>      Seq ID: 318O13_region_A3__36529_17

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cctgtagttg                                                          130


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<223>      Seq ID: 318O13_region_A3__139128_12

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gaacttcact gg                                                       132


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gaatatatgt aagctccagg tccaaacaaa caaaccaata ataagttaat aacatcagag  120

aatgaccgca aa                                                       132
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ggatccagta ag                                                       132
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tatacatatt ttgcctcgca cccattaaag agttggggtc ataatgtaat ttcgggacta  120

gaagtgcttt aggg                                                     134
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catggtggaa caaa                                                     134
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<212>      DNA
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<223>      Seq ID: 318O13_region_A3__3412_11

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cagttcaggg attcaaaaaa aaaaaaaaaa accagagaga gagaaagtga aaaaggtgtt   120

ggctttggtt aaggtt                                                   136


<210>      194
<211>      137
<212>      DNA
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<223>      Seq ID: 318O13_region_A3__276495_28

<400>      194

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ggctacacgt tgcagct                                                  137


<210>      195
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<223>      Seq ID: 318O13_region_A3__151839_17

<400>      195

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cctcctcttc ctcttcctg                                                139


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<400>      196

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agagaggaat tggagaagtg g                                           141


<210>     198
<211>     141
<212>     DNA
<213>     Glycine max

<223>     Seq ID: 318O13_region_A3__65193_11

<400>     198

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ctggtttgga agaacagcat a                                           141


<210>     199
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<223>     Seq ID: 318O13_region_A3__110573_70

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cacataaata ttatatccag cgtcagcgtt atcctcttct tcaaagggat tgacttcccg  180

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ggagaacatg aagaagacaa cgagccag                                       148


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agatagctac tacttcactt tcatcctttg ctccag                             156


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970

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973

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attgcgtttg ct                                                       192


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<223>      Seq ID: 318O13_region_A3__350540_17

<400>      302

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<223>   Seq ID: 318013_region_A3__453879_15

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aaactagtgt cttccactga aaaacttata tttaaaaata aaataaaatt gtcctttctt 180

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<223>   Seq ID: 318013_region_A3__201246_13

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<223>   Seq ID: 318013_region_A3__326020_13

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<223>   Seq ID: 318013_region_A3__503801_14

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ctccaatgtc ttacattttt cgctgatttt attttatttc caatttgtct ttcctcagat  180

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caacctgaat aggtaagaat aaataagaaa aataaaaagg atttgtggtt ttgcacaata  120

tatatatata tatatatata tatatatata tatatatata tatatatg gattcaacaa    180

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<223>     Seq ID: 318013_region_A3__448857_15

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aaattctagg ctgttaaaag tattttggaa agtgttattg ttttcttttc taaattgtat  180

ccaaggtggt ttgagggttt                                               200
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978

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<223>     Seq ID: 318013_region_A3__382583_13

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<223>     Seq ID: 318013_region_A3__124737_14

<400>     312

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tcctactaag tggggtcaac tgcatatgta tttcacaata aataaataaa aaatacttac  120

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ttgtgtattg gcaccaaaga ggacta                                       206
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<223>      Seq ID: 318O13_region_A3__124766_13

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tcctactaag tggggtcaac tgcatatgta tttcacaata aataaataaa aaatacttac  120

caatatattt atttatttct acattttaaa tttaaaatta ggacatttgc tcaacacaaa  180

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<223>      Seq ID: 318O13_region_A3__461351_16

<400>      314

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cgcaccacaa tgttcatcat catcatcatg ctcccaacta ctattaacac tagagaaacc  180

actttgctg cccttcaaca aattactat                                    209


<210>      315
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<212>      DNA
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<223>      Seq ID: 318O13_region_A3__64953_19

<400>      315

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acaccccaga aagacaaaaa cttttcataa gaaaagcacc aagtaacaa aataatataa  120

taacataata atggaatatg gaaaggaaaa gagagagaag aagaggaaga agaaaggggg  180

gaaaagagga tgagggcagt gaccctttaa agag                              214


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<223>      Seq ID: 318013_region_A3__366586_13

<400>      316

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agtattccaa tagatgtcgg tagaaaaaaa tcatccaaatt gataaagaaa aatctaaaat  180

catacatctt agacaaataa cgcatgtttg cattc                             215


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<212>      DNA
<213>      Glycine max

<223>      Seq ID: 318013_region_A3__46190_15

<400>      317

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aaaatcctct ctataaaaaa atcaataatt cacctctaaa aaaaaacaaa agtgaatcat  180

gaatgaatga atgtgtacct tggcctagcc tgaactt                           217


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<223>      Seq ID: 318013_region_A3__81016_11

<400>      318

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tctaaaatgc aataaaaatg attgtttgtt gtttgcattt aaaaaacagc aaaacctttc  180

gtgctaaaat aaaacttacca aacaagatgg aatcaaggct                       220


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<212>      DNA
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<223>      Seq ID: 318013_region_A3__134426_14
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aaaagactac tgatgaggat aaatacataa aaaaaaatag ttattttacc atctaaaaac   120

attgttccat tgagtacact tcaaatttag agaaaggaaa attgagttga aataatgaaa   180

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<223>   Seq ID: 318O13_region_A3__292724_14

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atataaatata taatatatga ttttggggga agtacttttt tctttgtgtg ttctgtgttg   180

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<212>   DNA
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<223>   Seq ID: 318O13_region_A3__187096_17

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<212>   DNA
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<223>   Seq ID: 318O13_region_A3__381693_13

<400>   322

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tactggatct tgtgttttct tactatttat gtcagacatt gtcagcctgc aaaatgaaga  180

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<223>     Seq ID: 318013_region_A3__361286_33

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<213>     Glycine max

<223>     Seq ID: 318013_region_A3__482668_14

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ataattctct aaccaatcaa attttatggc acacttgtac gtaagtctga              230


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<213>     Glycine max

<223>     Seq ID: 318013_region_A3__128002_12

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agagagagag aggctgaatc tgtttttctgt tattgattga tgaatcactt attactatct  180
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<213>    Glycine max

<223>    Seq ID: 318O13_region_A3__499270_14

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atcatgaatc tgacaattaa ttatacagat cagaaaacga gtcttctgat tcaaatccc   239


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<212>    DNA
<213>    Glycine max

<223>    Seq ID: 318O13_region_A3__231650_12

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tggccccgtg gaccctcca agtgcaccgc cgccgggacc gggatcgccg gcggaaccgc  180

gtgcgctccg tcctcctttg tggtggtggc caaggacgcc gatgagagga aggtttccgg  240

tg                                                                242


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<223>    Seq ID: 318O13_region_A3__199851_13

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aaataaataa aaattgctag attttgattc tgccttctga aaaaggaagt gcacattagc  180

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aaataaataa aaattgctag attttgattc tgccttctga aaaggaagt gcacattagc    180

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attggaaccc t                                                        251


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<223>      Seq ID: 318O13_region_A3__374190_19

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ccatataaac attcattatt tagatcttgt ttgtataaac ttctatataa aaacttttag   180

ggggaagtaa aaagtaaaat acattgagct tctcttataa gttaaaagca ggctagacag   240

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ataaactgac aacagagtat aaattaaaat atctttattt atttatagaa attctctcaa   180
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<223>      Seq ID: 318O13_region_A3__108681_14

<400>      332

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aaaaaaacat gattagtctt gacacataag ataaacatta atttaattta aaaaacaaag  180

aaaaaagtgt agagggggaga catatatttg acattttttta tttcaaaaga ataagagaaa  240

tatatatggt gcttgcatct tgatgaac                                     268


<210>      333
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<223>      Seq ID: 318O13_region_A3__459791_47

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atgtaaatgt cataaagagt tactgaataa gaatatatat atatatatat atatatatat  180

atatatatat atatatataa tatacattct taacatttaa tgttcaacaa gttaactgaa  240

taataataga ggtacctact cgcctcgga                                    269


<210>      334
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<212>      DNA
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<223>      Seq ID: 318O13_region_A3__4257_20

<400>      334

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atatattta gaaaaaatg atattaaaaa agttaaattc taaaataaaa taagacttgc  240

taaataaaaa gattagggag tggttacatt caagtttca                        279


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<212>      DNA
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<223>      Seq ID: 318O13_region_A3__238810_14

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taatttgata aaatcaattt tattattatt ttacaagcaa aaaaataagt aatgttatgt  180

taaaaaatta aaacaataat tattttgaaa cttattttg ttttacacga taattaatga  240

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<212>      DNA
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<223>      Seq ID: 318O13_region_A3__245817_14

<400>      336

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tctttttaaa ttttttttat tttatttttc atcctcaaaa tgatttagat aacaaagaaa  180

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<223>      Seq ID: 318O13_region_A3__245956_14

<400>      337

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agatatttat ttatttagct aaattgatct aaacacgcag aatggtagt               289


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<212>      DNA
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<223>      Seq ID: 318013_region_A3__74148_14

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cttttagttt gtgattgatt ttgattaact ataaaataaa ttaatttcaa cacctattca  180

gtgtgtactttg tacacttatg ttaatttatt ttagagattt tcttttttcta caatttctta  240

agtgagttaa aaaaatgttg attatttctt catacactct tgcagtgtg              289


<210>      339
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<223>      Seq ID: 318013_region_A3__74089_15

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cttttagttt gtgattgatt ttgattaact ataaaataaa ttaatttcaa cacctattca  180

gtgtgtactttg tacacttatg ttaatttatt ttagagattt tcttttttcta caatttctta  240

agtgagttaa aaaaatgttg attatttctt catacactct tgcagtgtg              289


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caacttttaa gaataataaa agatgtaact tatagaaatg gttttctcat aactattaaa  180

aacaacttt taaatagtta taaaaaagtg gacttaatta ttattatttt aaggagaact  240

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ttaaactaag atataacttt aatcttctta ttttgttaat tcactatttt ttatctaatt  120

taaaattgag acgtttagtt ttcaggtttc gaaaatctct aattttagtt cgatcttgaa  180

ttttgtcttc atttaatatt attattataa gagaccaaaa cacaaataat atatgtattt  240

aaacctttat tttatgatca aaatatatgt ttgcaaacct gggcacataa tggaacac     298
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<223>      Seq ID: 318O13_region_A3__164550_12

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tttttataact gatgaaaata tcaaatattt ctcccgctac atattttttat ttacctgaac  180

tcaacaaaac aaaaccttac gtatgagttt aaatgtacta atcgactaga gagagagagg  240

aaaaaaaag ataaaaatag aaataaatag acatttttat tcccggagga ccatatgtc    299
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<223>      Seq ID: 318O13_region_A3__101255_15
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gaatatattt ttgagttata tatatatata ttagtagtcc tacctcgttc taatatttta   180

tatttttttta ataaaatata caaattttta aacaattttg tattaaggaa aaattaatca   240

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<223>   Seq ID: 515002_region_G2__16189_11

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<210>   345
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<223>   Seq ID: 515002_region_G2__71925_13

<400>   345

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<223>   Seq ID: 515002_region_G2__4707_12

<400>   346

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<223>      Seq ID: 515O02_region_G2__118904_18

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<223>      Seq ID: 515O02_region_G2__13655_17

<400>      348

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ccacaggagc tt                                                       132


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<223>      Seq ID: 515O02_region_G2__53900_13

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aacaaacaaa agcaatttaa aaccatagaa tagaacacaa cacccaataa agagcataaa   120

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<223>      Seq ID: 515O02_region_G2__8079_14

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gcaagaggga agagagacag agatc                                         145
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<223>      Seq ID: 515O02_region_G2__9969_28

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tgagaaggaa acagtagctg gtagcg                                        146


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<223>      Seq ID: 515O02_region_G2__99475_19

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gagggtaatc gaagattcct gactcaa                                        147


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<223>      Seq ID: 515O02_region_G2__118615_18

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acaaacttaa ttttagttta gaacttattt ttacttagat ctttatatat atatatatat  120

acaacttagc gcccatacat acaatca                                      147
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<223>      Seq ID: 515O02_region_G2__119001_46

<400>      355
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tatatatata gatagataga tagatagata gatgatataga tagatagata gatagacatg  120

tacagcataa tcaagttgac caaatgcct                                     149
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<213>      Glycine max

<223>      Seq ID: 515O02_region_G2__118958_43

<400>      356
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tatatatata gatagataga tagatagata gatgatagata tagatagata gatagacatg  120

tacagcataa tcaagttgac caaatgcct                                     149
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<213>      Glycine max

<223>      Seq ID: 515O02_region_G2__17197_13

<400>      357
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ataaaggttt catcggactc ggtattatg                                     149
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<223>      Seq ID: 515O02_region_G2__105163_29

<400>      358

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ataagatggg aatgcatagg tacaaatgtt                                     150


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<223>      Seq ID: 515O02_region_G2__111335_13

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ctgagggctt tgagctcact gtggtctaat agacctcgtg aacctgctta gtctcacaac  120

aaggttacaa gagcgcaaac tcataacatg a                                   151


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<400>      360

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atgattactg gtactttctt ctggcagttg tt                                  152


<210>      361
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<223>      Seq ID: 515O02_region_G2__59229_17

<400>      361

gcttgtcagg agagaaatgt tgcttaaaaa gaaaagaaaa gaatgaacga cgctaaaact   60

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ttgacccact cccatgtttc atttgctgaa tt                              152
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cttcaacata tttatagtag tactatatag ttaaaacaaa accacctaat tattttttct  120
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<223>    Seq ID: 515O02_region_G2__36921_17

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aatcgccaaa gagaaaaaga accctcaacc aaacaacaac aacaacaaaa aaaaagcccct  120
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agaaaagatt ttggagaagc aatttctcac tcct                            154
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<223>    Seq ID: 515O02_region_G2__124150_19
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tataattatt gtttattttt ctttctttct ttctttttca ttttttaatg acatcttttt  120

ccattgttgt aatggcagaa atcagtgttc agtga                             155


<210>      366
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<213>      Glycine max

<223>      Seq ID: 515002_region_G2__5089_14

<400>      366

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tagttgaaaa aaaaattcag tttcatttta ttatttattt attttttcatc aagtggtaat 120

atgacatacg gagtgttgcc tcaacctgtc ttgttatg                          158


<210>      367
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<223>      Seq ID: 515002_region_G2__58221_15

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tcacttttag cattttcttt gctttctcca tttccatg                          158


<210>      368
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<212>      DNA
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<223>      Seq ID: 515002_region_G2__96139_14

<400>      368

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tttttcgtc agcttgaatg acacttggat ttgacaaag gtttttcat aataattata    120

ataataataa ttttcacgta aggttgagca taggacgagt t                      161
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<223>      Seq ID: 515002_region_G2__70595_13

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atattttttt aatgtgatgg aaaaaagaag ataagaagaa aaatcaggtg agatgataca   120

agaatatata tatataataa ttccaaatga aataccacaa aca                     163


<210>      370
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<223>      Seq ID: 515002_region_G2__4340_15

<400>      370

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ttcctccacc ccctctcttt tcccttccct ccttctcata tccaaa                  166


<210>      371
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<212>      DNA
<213>      Glycine max

<223>      Seq ID: 515002_region_G2__90417_11

<400>      371

aaactgcaaa cacaaattgc ctaaaataaa attgacaaac atgtaaactc ttttcatcac    60

cgaatagggt aatgggtagc caagagagag agataactga agggtaagaa tcagcagaaa   120

tcatcagaaa ggatatgaaa tgttaccaag tcaagtacag gctaccagg                169


<210>      372
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<212>      DNA
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<223>      Seq ID: 515002_region_G2__49711_17

<400>      372

caaagagagg cagaggaggt gattagatta gtgtcaactt gttgctatgc caacaatgac    60
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tatatctaga gtagtactcc tacaatcaaa tgacaagcag ctacaacca              169


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<223>      Seq ID: 515002_region_G2__63053_13

<400>      373

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ttatttgaaa gcaaatttat ttatgctgtt agtaaagatt gcagcaaga              169


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<223>      Seq ID: 515002_region_G2__63076_14

<400>      374

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ttatttgaaa gcaaatttat ttatgctgtt agtaaagatt gcagcaaga              169


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<212>      DNA
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<223>      Seq ID: 515002_region_G2__44442_12

<400>      375

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<212>      DNA
<213>      Glycine max
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gagtacaaaa tttatttctg gaatctgagg tgtttcatat agccatgttg c             171


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<213>     Glycine max

<223>     Seq ID: 515O02_region_G2__44158_19

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cgtagaaata ataataataa taaaaataaa taaataaata aataaagta ttttttgaaa    120

aataaaagat tgttagtact agttactacg gagtatcgta ttcgtatcat ccacccctg    178


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<223>     Seq ID: 515O02_region_G2__44141_17

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cgtagaaata ataataataa taaaaataaa taaataaata aataaagta ttttttgaaa    120

aataaaagat tgttagtact agttactacg gagtatcgta ttcgtatcat ccacccctg    178


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<223>     Seq ID: 515O02_region_G2__90762_17

<400>     379

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tctttacttt tctctattaa tatttttta aaaagaaaat tcttctcaca tatacaaaga    120

gtcttgaggg agggagggag ggcaatgccc ccccttgaat ccgttaccac agggtaat     178
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<213>      Glycine max

<223>      Seq ID: 515O02_region_G2__106241_14

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aacgttttct caaagtggtt tttttatttt attttttttta tcataaggtt tggctttta   120

gttttttatt tttcagtttt tgtggataat tctattaact gtcaagggag gaaattggta   180

ca                                                                  182


<210>      381
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<212>      DNA
<213>      Glycine max

<223>      Seq ID: 515O02_region_G2__109676_12

<400>      381

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tcttcttgag agagagagat gggggaaatt tgaaactgca ttcatttatt acagttttaa   120

tacattatgc aagatttact caaatgcttt ttgtacttaa aatggctatc actcagtgtc   180

agtga                                                               185


<210>      382
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<223>      Seq ID: 515O02_region_G2__86242_14

<400>      382

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tagcaaaaaa aaatagaaaa actaagcata ctaaaacatt atcattttaa gaaagaaaga   120

aaaaagacta tcataactga ttaggatcat aaaatttcct gaaactccaa atttcttctt   180

tgtgc                                                               185


<210>      383
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<213>      Glycine max

<223>      Seq ID: 515O02_region_G2__83109_12

<400>      383

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aaaagtctga aatcttttg agttcgatta ttcaacaaca acaaagacac aaaatctctt   120

cctaggtgtc actaaaagca ttggatccaa caaatattta ggacttcctt caatcattgg   180

caagag                                                              186


<210>      384
<211>      192
<212>      DNA
<213>      Glycine max

<223>      Seq ID: 515O02_region_G2__10461_15

<400>      384

ggctgtgtgt gagtgagagt gagagtgaga gtgagggtgg ataaaacaaa caaacaaaac   60

tagcgcattt tgttgcgggt ggaattagac tgttactaag tgcttaatta atggggaaag   120

gaaagtggta tgattagtgt ttgtaacagt aagtgattat tgtaaatgat gattaggagg   180

aataagggtg ca                                                       192


<210>      385
<211>      194
<212>      DNA
<213>      Glycine max

<223>      Seq ID: 515O02_region_G2__67608_15

<400>      385

ggtggttaga tccaatttca tgttgaattt aatattgtgg aacaaaaagg cggtgttata   60

tatatatata tgatggtcga tggtgcaaga ggggatcgga agattatact taaagaagca   120

gaagcatact tgtactccaa tctaataaaa atgttctata tataatagaa aatacggata   180

cgtgctgtac agga                                                     194


<210>      386
<211>      200
<212>      DNA
<213>      Glycine max

<223>      Seq ID: 515O02_region_G2__63275_46
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tgccctgcat gtacatttta ttattagttt gtttgatgat tttggaattt tgtggtttaa   120

tttattaata tatatatata tatatatata tatatatata tatatgtata tattttgaag   180

gaattgagga gcggagtata                                               200


<210>      387
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<212>      DNA
<213>      Glycine max

<223>      Seq ID: 515O02_region_G2__62405_14

<400>      387

tgcatagaga gaaatagacg aggaaaaata taaaagaaaa gaaaaaaatt ataaataaaa   60

caaacaacat aataaaaaat gaaaagaaga atagaaggaa aaatagactc aaaatgagat   120

tttgaaatta tataattaat aatccaatta atctcatgag atattattct ataactataa   180

cttatggacc gtttggaaga gat                                           203


<210>      388
<211>      211
<212>      DNA
<213>      Glycine max

<223>      Seq ID: 515O02_region_G2__33563_12

<400>      388

ccttaggtgc tcatacatcc aaacacttac acacttgttt tagtaaataa tgttatattc   60

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ctcatttata aattattgtc aaagataatt ttgttgaaca aatttttaa atatttacaa    180

aatatacgtt tcttgcgttg tatatgaatc a                                  211


<210>      389
<211>      243
<212>      DNA
<213>      Glycine max

<223>      Seq ID: 515O02_region_G2__33146_14

<400>      389

cgaaccctaa acatttcaaa ccaaattact cacagatata gtttttttca aaaattgatt   60
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gagagatcgt gtagaaaaag taaatttcaa gcaaaactca tcctcaatat cctttttgta  120

ttggtttata aacatgagag aattgggaaa acgcttttgt tttttgatcc attctcacat  180

ctgcgatttt gcttcttttt ctttctttct tccatgtatg tgtttccaac ctttcttctg  240

aaa                                                               243


<210>      390
<211>      251
<212>      DNA
<213>      Glycine max

<223>      Seq ID: 515002_region_G2__102179_29

<400>      390

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taaattatat tgacaactat atatatatat atatatatat atatattatg taacaaattt  120

tatgatgcag ttagataaca agaatcaaac aataaaaata tataaaaata agcttaagta  180

attaatatcc ctaaaattaa atcagataaa ttaaaatggt ttgtatattg cttgattgtt  240

gacttgttgg a                                                      251


<210>      391
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<212>      DNA
<213>      Glycine max

<223>      Seq ID: 515002_region_G2__2646_15

<400>      391

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aaaataagat aaatcaattt tttcacaagt taaattttat tttatttttt ggaattttta  120

caagaaataa aaaaattcat aacttaaaat taactcatgt atgataactt tttaatagtt  180

ttttgttta attttcctaa aagataaggc gtataaatta attttagttt acgagagaag  240

ttggatttgt ttatttc                                                257


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<213>      Glycine max

<223>      Seq ID: 515002_region_G2__76652_24

<400>      392
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taagagaata taaaaaaatt atgaatagta taattttttg tttttcaatt tttaaaattt  180

taattaaagg aaaattggtt atatttaaaa ttattcttta tgtagaagaa aaattgataa  240

atgattttga tccagtatat gtcccaggg                                     269


<210>      393
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<223>      Seq ID: 515O02_region_G2__66280_14

<400>      393

gtgttagatt gattaaagtt cgctgatata acttttattt aatgaaaatt aaattgttag   60

tacaaatatt gcaagtcttt attaataata caatacatca tactaacata tccaaaatat  120

ttatactaat taacagttca atcctgctag ataaatgctt ttctatatat acactgacag  180

aacagtttta atgctttttt aattttttcc tgtttgtaat aatgattttt tgtttgtttg  240

ttagaaattg acatttttt cactttaatc atgggctaaa tct                     283


<210>      394
<211>      284
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<223>      Seq ID: 515O02_region_G2__54768_13

<400>      394

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tatactacta ttcgtattat tatcaaatat taatatgttc catagaaatt tacaaattat  120

ttatattcta ttattattat ttagtaatag tagtatagta ttagtaatga cattggatcg  180

taaatgtaaa ttaaatatta tatcattagt atttgtagga atgtaaaatt taatttaaat  240

gaaaaaatatt atatgacaaa agttatggtg caatattgtg cctg                   284


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<213>      Glycine max

<223>      Seq ID: 515O02_region_G2__62580_14
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aacttttctt atgttttaac ttttttttaa tttcaaattt tccttttctt gattttcttt  180

tcccactaca attgactgag tcagactgaa cgtgatactt agatacatac atgcaactct  240

cagtactact cctcacctct atataatctt cactctttgc tcctcctttt               289


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<223>      Seq ID: 515002_region_G2__34598_55

<400>      396

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cttattaaat taaatagatc agacttaggc ttgttaaaaa gccttataag tctgataggt  120

cggcctatat atatatatat atatatgtat atgtatatat atatatatat gtatatatat  180

ttatattatt tgttgatacc aatttatact tatattattt tttgggtaca attaattttt  240

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<223>      Seq ID: 515002_region_G2__77680_13

<400>      397

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ccccttaaa atttggcttt caaaaagtac tttttttcaaa atacattaat ttttaacatg  120

gctagaaagt atttttgaaa tattaaaaatt ttaacacttc cagaaaatat tttctgaaat  180

gtgttgaaat tttttaatct gttttgaaaa gtagtttcca aaaaagagat acttgtagaa  240

gaagaagaat atatatatat agtattagta aatctgggag gtgtaaataa cagttgtt    298


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<223>      Seq ID: 515O02_region_G2__77693_12

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cccccttaaa atttggcttt caaaaagtac tttttttcaaa atacattaat ttttaacatg  120

gctagaaagt attttttgaaa tattaaaaatt ttaacacttc cagaaaaatat tttctgaaat  180

gtgttgaaat tttttaatct gttttgaaaa gtagtttcca aaaaagagat acttgtagaa  240

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<223>      Seq ID: 515O02_region_G2__97392_14

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aaatgggttt tggggatttc acttacttaa tatgatttag aaacattatt attattattt  120

ctgtaaaaaa aaagaaatat tattattatt acaatttctt catccttctt atatacttttt  180

ttaaaaacga aaaaaaaaaa tattgagttt cgtttatgat taagaaaaat gtttcataat  240

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<223>      Seq ID: 515O02_region_G2__97359_15

<400>      400

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aaatgggttt tggggatttc acttacttaa tatgatttag aaacattatt attattattt  120

ctgtaaaaaa aaagaaatat tattattatt acaatttctt catccttctt atatactttt  180

ttaaaaacga aaaaaaaaaa tattgagttt cgtttatgat taagaaaaat gtttcataat  240

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<223>      Seq ID: 240017_region_G3__289711_11_Forward_Primer

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<223>      Seq ID: 240017_region_G3__289711_11_Reverse_Primer

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<223>      Seq ID: 240017_region_G3__236585_14_Forward_Primer

<400>      403

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<223>      Seq ID: 240017_region_G3__236585_14_Reverse_Primer

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<223>      Seq ID: 240017_region_G3__168772_13_Forward_Primer

<400>      405

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<223>     Seq ID: 240O17_region_G3__332420_21_Forward_Primer

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<223>     Seq ID: 240O17_region_G3__332420_21_Reverse_Primer

<400>     408

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<223>     Seq ID: 240O17_region_G3__228126_18_Forward_Primer

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<223>     Seq ID: 240O17_region_G3__228126_18_Reverse_Primer

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<223>    Seq ID: 240017_region_G3__139723_11_Forward_Primer

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<400>    412

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<223>    Seq ID: 240017_region_G3__280585_14_Forward_Primer

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<223>   Seq ID: 240017_region_G3__50537_17_Forward_Primer

<400>   417

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<223>   Seq ID: 240017_region_G3__50537_17_Reverse_Primer

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<223>   Seq ID: 240017_region_G3__231556_17_Forward_Primer

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<223>   Seq ID: 240017_region_G3__231556_17_Reverse_Primer

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<223>    Seq ID: 240017_region_G3__117057_11_Forward_Primer

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aaagacggaa cagcgtcaaa taaac                              25


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<400>    422

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<223>    Seq ID: 240017_region_G3__23092_13_Forward_Primer

<400>    423

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<223>    Seq ID: 240017_region_G3__23092_13_Reverse_Primer

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<210>    426
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<223>    Seq ID: 240O17_region_G3__297741_14_Reverse_Primer

<400>    426

agaactagat tggtatgccc gtgct                                    25


<210>    427
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<223>    Seq ID: 240O17_region_G3__206502_14_Forward_Primer

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<223>    Seq ID: 240O17_region_G3__206502_14_Reverse_Primer

<400>    428

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<223>    Seq ID: 240O17_region_G3__221223_13_Forward_Primer

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<212>      DNA
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<223>      Seq ID: 240O17_region_G3__221223_13_Reverse_Primer

<400>      430

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<223>      Seq ID: 240O17_region_G3__169084_14_Forward_Primer

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<210>      432
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<223>      Seq ID: 240O17_region_G3__169084_14_Reverse_Primer

<400>      432

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<210>      433
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<223>      Seq ID: 240O17_region_G3__94891_14_Forward_Primer

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<223>      Seq ID: 240O17_region_G3__94891_14_Reverse_Primer

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1013

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<400>    436

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<223>    Seq ID: 240017_region_G3__281852_61_Forward_Primer

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aaccagagga aacagggagt cattt                                    25


<210>    438
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<223>    Seq ID: 240017_region_G3__281852_61_Reverse_Primer

<400>    438

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<223>    Seq ID: 240017_region_G3__46583_12_Forward_Primer

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<223>     Seq ID: 240O17_region_G3__46583_12_Reverse_Primer

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<223>     Seq ID: 240017_region_G3__306835_13_Forward_Primer

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<223>     Seq ID: 240017_region_G3__306835_13_Reverse_Primer

<400>     442

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<223>     Seq ID: 240017_region_G3__85471_12_Forward_Primer

<400>     443

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<210>     444
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<223>     Seq ID: 240017_region_G3__85471_12_Reverse_Primer

<400>     444
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<223>      Seq ID: 240017_region_G3__257208_12_Forward_Primer

<400>      445

ccatgaatga aactcaccaa actga                                      25


<210>      446
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<223>      Seq ID: 240017_region_G3__257208_12_Reverse_Primer

<400>      446

aattactatg attctggctg gcaca                                      25


<210>      447
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<213>      Glycine max

<223>      Seq ID: 240017_region_G3__150390_17_Forward_Primer

<400>      447

ttacgcactc agatttggat ttgat                                      25


<210>      448
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<223>      Seq ID: 240017_region_G3__150390_17_Reverse_Primer

<400>      448

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<210>      449
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<223>      Seq ID: 240017_region_G3__34697_75_Forward_Primer
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<400>   449

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<210>   450
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<223>   Seq ID: 240017_region_G3__34697_75_Reverse_Primer

<400>   450

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<210>   451
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<223>   Seq ID: 240017_region_G3__150374_13_Forward_Primer

<400>   451

ttacgcactc agatttggat ttgat   25

<210>   452
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<223>   Seq ID: 240017_region_G3__150374_13_Reverse_Primer

<400>   452

agggtgtgaa gtttaatcac catga   25

<210>   453
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<223>   Seq ID: 240017_region_G3__40513_22_Forward_Primer

<400>   453

attctgaaat tggtggaagg ttctg   25

<210>   454
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<223>   Seq ID: 240017_region_G3__40513_22_Reverse_Primer

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caaataaatg tgaagccaca cctga   25

<210>   455
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<212>   DNA
<213>   Glycine max

<223>   Seq ID: 240017_region_G3__268602_14_Forward_Primer

<400>   455

aacacgtctc atctcaagaa gctca   25

<210>   456
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<223>   Seq ID: 240017_region_G3__268602_14_Reverse_Primer

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<210>   457
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<212>   DNA
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<223>   Seq ID: 240017_region_G3__25357_13_Forward_Primer

<400>   457

acttctccca cactttccct ttctc   25

<210>   458
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<212>   DNA
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<223>   Seq ID: 240017_region_G3__25357_13_Reverse_Primer

<400>   458

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<210>   459
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    <223>      Seq ID: 240O17_region_G3__137548_13_Forward_Primer

    <400>      459

gtatgaaccc taaagctggc ttcg                                    24


    <210>      460
    <211>      25
    <212>      DNA
    <213>      Glycine max

    <223>      Seq ID: 240O17_region_G3__137548_13_Reverse_Primer

    <400>      460

gcacagattt gttaagagga atgct                                   25


    <210>      461
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    <212>      DNA
    <213>      Glycine max

    <223>      Seq ID: 240O17_region_G3__139131_13_Forward_Primer

    <400>      461

gtatgaaccc taaagctggc ttcg                                    24


    <210>      462
    <211>      25
    <212>      DNA
    <213>      Glycine max

    <223>      Seq ID: 240O17_region_G3__139131_13_Reverse_Primer

    <400>      462

gcacagattt gttaagagga atgct                                   25


    <210>      463
    <211>      25
    <212>      DNA
    <213>      Glycine max

    <223>      Seq ID: 240O17_region_G3__203855_12_Forward_Primer

    <400>      463

ttgttgtcaa gagaagggaa gctct                                   25
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<223>      Seq ID: 240O17_region_G3__203855_12_Reverse_Primer

<400>      464

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<210>      465
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<223>      Seq ID: 240O17_region_G3__199049_15_Forward_Primer

<400>      465

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<210>      466
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<223>      Seq ID: 240O17_region_G3__199049_15_Reverse_Primer

<400>      466

tcaccaaata aactcactga gcaaa                                        25


<210>      467
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<212>      DNA
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<223>      Seq ID: 240O17_region_G3__320907_12_Forward_Primer

<400>      467

gattcgccgg aaattctctc ct                                           22


<210>      468
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<212>      DNA
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<223>      Seq ID: 240O17_region_G3__320907_12_Reverse_Primer

<400>      468

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<223>     Seq ID: 240017_region_G3__16407_17_Forward_Primer

<400>     469

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<210>     470
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<223>     Seq ID: 240017_region_G3__16407_17_Reverse_Primer

<400>     470

atatcactga tccacgtggg atttc                                    25


<210>     471
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<212>     DNA
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<223>     Seq ID: 240017_region_G3__206516_17_Forward_Primer

<400>     471

cagaagacga agacgaagaa gagga                                    25


<210>     472
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<223>   Seq ID: 240O17_region_G3__214106_13_Forward_Primer

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tccaaaccct tattcataac ccaga                                      25


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<223>     Seq ID: 240017_region_G3__143975_14_Reverse_Primer

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<400>      508

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<223>      Seq ID: 240017_region_G3__225343_17_Forward_Primer

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<223>      Seq ID: 240017_region_G3__225343_17_Reverse_Primer

<400>      510

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<223>      Seq ID: 240017_region_G3__208823_14_Forward_Primer

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<223>   Seq ID: 240O17_region_G3__208823_14_Reverse_Primer

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tatgcgtatt acctccaacg tccat                                        25


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tgaaatccaa gtgaaagatt gttaaa                                       26
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<223>      Seq ID: 240O17_region_G3__35078_13_Reverse_Primer

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<223>      Seq ID: 240O17_region_G3__210506_16_Forward_Primer

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<223>      Seq ID: 240O17_region_G3__229651_18_Forward_Primer

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acaatcaagg aatctaagcc acaca                                    25


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<223>      Seq ID: 240O17_region_G3__229651_18_Reverse_Primer

<400>      538

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<223>      Seq ID: 240O17_region_G3__303308_19_Forward_Primer

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<223>      Seq ID: 240O17_region_G3__303308_19_Reverse_Primer

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<210>      554
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<210>      555
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<400>      555

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1038

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tttccacaaa gactcctgcc cttt                                       24


<210>      560
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<223>   Seq ID: 240017_region_G3__88478_19_Forward_Primer

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<223>      Seq ID: 318013_region_A3__111684_19_Forward_Primer_Seq

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<223>      Seq ID: 318013_region_A3__111684_19_Reverse_Primer_Seq

<400>      666

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<400>      667

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<223>      Seq ID: 318O13_region_A3__69328_14_Reverse_Primer_Seq

<400>      668

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<223>      Seq ID: 318O13_region_A3__36529_17_Reverse_Primer_Seq

<400>      670

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<223>      Seq ID: 318O13_region_A3__139128_12_Forward_Primer_Seq

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<223>      Seq ID: 318O13_region_A3__453036_14_Forward_Primer_Seq

<400>      677

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<223>      Seq ID: 318O13_region_A3__453036_14_Reverse_Primer_Seq

<400>      678

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<223>      Seq ID: 318O13_region_A3__374041_13_Forward_Primer_Seq

<400>      679

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<400>      680

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<210>      682
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<223>      Seq ID: 318O13_region_A3__3412_11_Reverse_Primer_Seq

<400>      682

aaccttaacc aaagccaaca ccttt                                        25


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<223>      Seq ID: 318O13_region_A3__276495_28_Forward_Primer_Seq

<400>      683

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<223>      Seq ID: 318O13_region_A3__276495_28_Reverse_Primer_Seq

<400>      684

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<223>      Seq ID: 318O13_region_A3__151839_17_Forward_Primer_Seq

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<400>     689

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<223>     Seq ID: 318013_region_A3__104560_12_Reverse_Primer_Seq

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<400>       691

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<400>       692

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<223>       Seq ID: 318O13_region_A3__110573_70_Forward_Primer_Seq

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<223>       Seq ID: 318O13_region_A3__65117_12_Forward_Primer_Seq

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<223>      Seq ID: 318O13_region_A3__490837_16_Reverse_Primer_Seq

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<400>    701

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<400>    702

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<210>    703
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<223>    Seq ID: 318O13_region_A3__193470_13_Forward_Primer_Seq

<400>    703

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<210>    704
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<223>    Seq ID: 318O13_region_A3__193470_13_Reverse_Primer_Seq

<400>    704

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<223>    Seq ID: 318O13_region_A3__183305_14_Forward_Primer_Seq
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<400>   705

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<400>   706

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<223>   Seq ID: 318O13_region_A3__4654_22_Forward_Primer_Seq

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<210>   714
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<223>   Seq ID: 318O13_region_A3__4654_22_Reverse_Primer_Seq

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<223>      Seq ID: 318O13_region_A3__408959_13_Forward_Primer_Seq

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<210>      716
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<223>      Seq ID: 318O13_region_A3__408959_13_Reverse_Primer_Seq

<400>      716

gtgtagttag cgtggtctgc ttgtg                              25


<210>      717
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<223>      Seq ID: 318O13_region_A3__132288_22_Forward_Primer_Seq

<400>      717

acaggtcatc taaccaattg catgt                              25


<210>      718
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<212>      DNA
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<223>      Seq ID: 318O13_region_A3__132288_22_Reverse_Primer_Seq

<400>      718

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<210>      719
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<400>      719

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<400>      722

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<210>      723
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<223>      Seq ID: 318O13_region_A3__509623_13_Forward_Primer_Seq

<400>      723

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<210>      724
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<400>      724

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1073

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<400>      725

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<223>      Seq ID: 318O13_region_A3__190404_14_Reverse_Primer_Seq

<400>      726

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<223>      Seq ID: 318O13_region_A3__164916_15_Forward_Primer_Seq

<400>      727

aggctacggt atagaccacg ttgaa                                    25


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<400>      728

gaatggaatt gatctttcca gaacc                                    25


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agtggcggac ctgattctcc   20

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<223>   Seq ID: 318O13_region_A3__484089_14_Forward_Primer_Seq

<400>   733

cgatcgcatg atagagttca ccaat   25

<210>   734
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<400>      734

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<210>      735
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<223>      Seq ID: 318013_region_A3__332780_17_Forward_Primer_Seq

<400>      735

gttacaacag ctacctccgc agact                                    25


<210>      736
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<223>      Seq ID: 318013_region_A3__332780_17_Reverse_Primer_Seq

<400>      736

agtggcggac ctgattctcc                                          20


<210>      737
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<223>      Seq ID: 318013_region_A3__480137_37_Forward_Primer_Seq

<400>      737

ttcaagggaa ggagaagaat agattt                                   26


<210>      738
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<223>      Seq ID: 318013_region_A3__480137_37_Reverse_Primer_Seq

<400>      738

tccctattaa gtttccttta atccatc                                  27


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<223>   Seq ID: 318O13_region_A3__441056_14_Forward_Primer_Seq

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<210>   740
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<223>   Seq ID: 318O13_region_A3__441056_14_Reverse_Primer_Seq

<400>   740

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<210>   741
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<223>   Seq ID: 318O13_region_A3__77486_11_Forward_Primer_Seq

<400>   741

atacccaaat cccatcttcc atttc   25

<210>   742
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<223>   Seq ID: 318O13_region_A3__77486_11_Reverse_Primer_Seq

<400>   742

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<210>   743
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<212>   DNA
<213>   Glycine max

<223>   Seq ID: 318O13_region_A3__272468_11_Forward_Primer_Seq

<400>   743

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<210>   744
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    <213>       Glycine max

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    <400>       744

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    <210>       745
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    <223>       Seq ID: 318O13_region_A3__425319_17_Forward_Primer_Seq

    <400>       745

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    <210>       746
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    <213>       Glycine max

    <223>       Seq ID: 318O13_region_A3__425319_17_Reverse_Primer_Seq

    <400>       746

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    <223>       Seq ID: 318O13_region_A3__413879_31_Forward_Primer_Seq

    <400>       747

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    <210>       748
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    <400>       748

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<223>     Seq ID: 318O13_region_A3__80477_64_Forward_Primer_Seq

<400>     749

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<210>     750
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<400>     750

gggaagtggg atagttgata gcaga                                    25


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<223>     Seq ID: 318O13_region_A3__277272_50_Forward_Primer_Seq

<400>     751

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<223>     Seq ID: 318O13_region_A3__277272_50_Reverse_Primer_Seq

<400>     752

tctgtcattg aacatgcaca acatt                                    25


<210>     753
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<223>     Seq ID: 318O13_region_A3__509642_13_Forward_Primer_Seq

<400>     753

ctaaacgctt tggtttcttc accac                                    25
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<223>      Seq ID: 318O13_region_A3__509642_13_Reverse_Primer_Seq

<400>      754

tcgatcaata tcctctctcc gaatc                                    25


<210>      755
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<223>      Seq ID: 318O13_region_A3__321771_14_Forward_Primer_Seq

<400>      755

atcaaactct ggaaacaggt tggtg                                    25


<210>      756
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<212>      DNA
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<223>      Seq ID: 318O13_region_A3__321771_14_Reverse_Primer_Seq

<400>      756

gtcagcaaca ccttggaatt aatgg                                    25


<210>      757
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<212>      DNA
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<223>      Seq ID: 318O13_region_A3__26788_12_Forward_Primer_Seq

<400>      757

gaagagacaa ttgtgaggca aatca                                    25


<210>      758
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<223>      Seq ID: 318O13_region_A3__26788_12_Reverse_Primer_Seq

<400>      758
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<223>     Seq ID: 318O13_region_A3__185019_12_Forward_Primer_Seq

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<223>   Seq ID: 318013_region_A3__381102_14_Forward_Primer_Seq

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<223>   Seq ID: 318013_region_A3__491826_15_Forward_Primer_Seq

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<223>    Seq ID: 318O13_region_A3__372628_15_Forward_Primer_Seq

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<223>   Seq ID: 318O13_region_A3__269358_15_Forward_Primer_Seq

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<223>      Seq ID: 318O13_region_A3__176598_14_Forward_Primer_Seq

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<223>      Seq ID: 318O13_region_A3__176598_14_Reverse_Primer_Seq

<400>      824

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<223>      Seq ID: 318O13_region_A3__278266_12_Forward_Primer_Seq

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<400>        832

ttcactccca attgtcatac aaaca                                     25


<210>        833
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<223>        Seq ID: 318O13_region_A3__315094_13_Forward_Primer_Seq

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<223>    Seq ID: 318013_region_A3__252426_85_Forward_Primer_Seq

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taacgctgca tgatttgagt tctgt   25

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1109

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<210>      996
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<223>      Seq ID: 515O02_region_G2__9969_28_Forward_Primer

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<400>      998

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<223>      Seq ID: 515002_region_G2__118615_18_Forward_Primer

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<223>    Seq ID: 515002_region_G2__119001_46_Reverse_Primer

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<223>    Seq ID: 515002_region_G2__118958_43_Forward_Primer

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<223>    Seq ID: 515002_region_G2__118958_43_Reverse_Primer

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<223>    Seq ID: 515002_region_G2__17197_13_Forward_Primer

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<223>     Seq ID: 515002_region_G2__105163_29_Forward_Primer

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<223>     Seq ID: 515002_region_G2__105163_29_Reverse_Primer

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<223>     Seq ID: 515002_region_G2__111335_13_Forward_Primer

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<223>    Seq ID: 515O02_region_G2__106396_13_Reverse_Primer

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<223>    Seq ID: 515O02_region_G2__59229_17_Forward_Primer

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    <223>     Seq ID: 515O02_region_G2__96139_14_Reverse_Primer

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<223>     Seq ID: 515O02_region_G2__90417_11_Forward_Primer

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aaactgcaaa cacaaattgc ctaaa                                     25


<210>     1038
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<223>     Seq ID: 515O02_region_G2__90417_11_Reverse_Primer

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<223>      Seq ID: 515O02_region_G2__49711_17_Reverse_Primer

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<223>      Seq ID: 515O02_region_G2__63053_13_Forward_Primer

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<210>      1042
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<212>      DNA
<213>      Glycine max

<223>      Seq ID: 515O02_region_G2__63053_13_Reverse_Primer

<400>      1042

tcttgctgca atctttacta acagca                                    26


<210>      1043
<211>      25
<212>      DNA
<213>      Glycine max

<223>      Seq ID: 515O02_region_G2__63076_14_Forward_Primer

<400>      1043
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tgtgcataac tcgatctctt gatga                              25


<210>    1044
<211>    26
<212>    DNA
<213>    Glycine max

<223>    Seq ID: 515002_region_G2__63076_14_Reverse_Primer

<400>    1044

tcttgctgca atctttacta acagca                             26


<210>    1045
<211>    25
<212>    DNA
<213>    Glycine max

<223>    Seq ID: 515002_region_G2__44442_12_Forward_Primer

<400>    1045

aacgcgtctt tctttcttct tcaac                              25


<210>    1046
<211>    25
<212>    DNA
<213>    Glycine max

<223>    Seq ID: 515002_region_G2__44442_12_Reverse_Primer

<400>    1046

gcaacatggc tatatgaaac acctc                              25


<210>    1047
<211>    25
<212>    DNA
<213>    Glycine max

<223>    Seq ID: 515002_region_G2__44422_19_Forward_Primer

<400>    1047

aacgcgtctt tctttcttct tcaac                              25


<210>    1048
<211>    25
<212>    DNA
<213>    Glycine max

<223>    Seq ID: 515002_region_G2__44422_19_Reverse_Primer
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1140

<400>   1048

gcaacatggc tatatgaaac acctc   25

<210>   1049
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<213>   Glycine max

<223>   Seq ID: 515OO2_region_G2__44158_19_Forward_Primer

<400>   1049

tttcattacg tgcgtttgta caacta   26

<210>   1050
<211>   26
<212>   DNA
<213>   Glycine max

<223>   Seq ID: 515OO2_region_G2__44158_19_Reverse_Primer

<400>   1050

cagggtggat gatacgaata cgatac   26

<210>   1051
<211>   26
<212>   DNA
<213>   Glycine max

<223>   Seq ID: 515OO2_region_G2__44141_17_Forward_Primer

<400>   1051

tttcattacg tgcgtttgta caacta   26

<210>   1052
<211>   26
<212>   DNA
<213>   Glycine max

<223>   Seq ID: 515OO2_region_G2__44141_17_Reverse_Primer

<400>   1052

cagggtggat gatacgaata cgatac   26

<210>   1053
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<212>   DNA
<213>   Glycine max

1141

<223>   Seq ID: 515O02_region_G2__90762_17_Forward_Primer

<400>   1053

ccagagatat gattcaatac aaaggaa   27

<210>   1054
<211>   25
<212>   DNA
<213>   Glycine max

<223>   Seq ID: 515O02_region_G2__90762_17_Reverse_Primer

<400>   1054

attaccctgt ggtaacggat tcaag   25

<210>   1055
<211>   25
<212>   DNA
<213>   Glycine max

<223>   Seq ID: 515O02_region_G2__106241_14_Forward_Primer

<400>   1055

tagatagcta gccatgttgg catga   25

<210>   1056
<211>   25
<212>   DNA
<213>   Glycine max

<223>   Seq ID: 515O02_region_G2__106241_14_Reverse_Primer

<400>   1056

tgtaccaatt tcctcccttg acagt   25

<210>   1057
<211>   26
<212>   DNA
<213>   Glycine max

<223>   Seq ID: 515O02_region_G2__109676_12_Forward_Primer

<400>   1057

tcattgtctt tgaggacttt ctcatt   26

<210>   1058
<211>   26

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        <212>    DNA
        <213>    Glycine max

        <223>    Seq ID: 515002_region_G2__109676_12_Reverse_Primer

        <400>    1058

tcactgacac tgagtgatag ccattt                                          26


        <210>    1059
        <211>    25
        <212>    DNA
        <213>    Glycine max

        <223>    Seq ID: 515002_region_G2__86242_14_Forward_Primer

        <400>    1059

ccacaactcc gatttatccc ataac                                           25


        <210>    1060
        <211>    26
        <212>    DNA
        <213>    Glycine max

        <223>    Seq ID: 515002_region_G2__86242_14_Reverse_Primer

        <400>    1060

gcacaaagaa gaaatttgga gtttca                                          26


        <210>    1061
        <211>    25
        <212>    DNA
        <213>    Glycine max

        <223>    Seq ID: 515002_region_G2__83109_12_Forward_Primer

        <400>    1061

tcacccttta ggagatccta gacac                                           25


        <210>    1062
        <211>    25
        <212>    DNA
        <213>    Glycine max

        <223>    Seq ID: 515002_region_G2__83109_12_Reverse_Primer

        <400>    1062

ctcttgccaa tgattgaagg aagtc                                           25
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1143

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<210>    1063
<211>    25
<212>    DNA
<213>    Glycine max

<223>    Seq ID: 515OO2_region_G2__10461_15_Forward_Primer

<400>    1063

ggctgtgtgt gagtgagagt gagag                                  25


<210>    1064
<211>    25
<212>    DNA
<213>    Glycine max

<223>    Seq ID: 515OO2_region_G2__10461_15_Reverse_Primer

<400>    1064

tgcaccctta ttcctcctaa tcatc                                  25


<210>    1065
<211>    26
<212>    DNA
<213>    Glycine max

<223>    Seq ID: 515OO2_region_G2__67608_15_Forward_Primer

<400>    1065

ggtggttaga tccaatttca tgttga                                 26


<210>    1066
<211>    25
<212>    DNA
<213>    Glycine max

<223>    Seq ID: 515OO2_region_G2__67608_15_Reverse_Primer

<400>    1066

tcctgtacag cacgtatccg tattt                                  25


<210>    1067
<211>    26
<212>    DNA
<213>    Glycine max

<223>    Seq ID: 515OO2_region_G2__63275_46_Forward_Primer

<400>    1067

tgctgttagt aaagattgca gcaaga                                 26
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<210>      1068
<211>      25
<212>      DNA
<213>      Glycine max

<223>      Seq ID: 515O02_region_G2__63275_46_Reverse_Primer

<400>      1068

tatactccgc tcctcaattc cttca                                    25


<210>      1069
<211>      26
<212>      DNA
<213>      Glycine max

<223>      Seq ID: 515O02_region_G2__62405_14_Forward_Primer

<400>      1069

tgcatagaga gaaatagacg aggaaa                                   26


<210>      1070
<211>      25
<212>      DNA
<213>      Glycine max

<223>      Seq ID: 515O02_region_G2__62405_14_Reverse_Primer

<400>      1070

atctcttcca aacggtccat aagtt                                    25


<210>      1071
<211>      25
<212>      DNA
<213>      Glycine max


<223>      Seq ID: 515O02_region_G2__33563_12_Forward_Primer

<400>      1071

ccttaggtgc tcatacatcc aaaca                                    25


<210>      1072
<211>      25
<212>      DNA
<213>      Glycine max

<223>      Seq ID: 515O02_region_G2__33563_12_Reverse_Primer
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<400>    1072

tgattcatat acaacgcaag aaacg                                    25


<210>    1073
<211>    25
<212>    DNA
<213>    Glycine max

<223>    Seq ID: 515OO2_region_G2__33146_14_Forward_Primer

<400>    1073

cgaaccctaa acatttcaaa ccaaa                                    25


<210>    1074
<211>    25
<212>    DNA
<213>    Glycine max

<223>    Seq ID: 515OO2_region_G2__33146_14_Reverse_Primer

<400>    1074

tttcagaaga aaggttggaa acaca                                    25


<210>    1075
<211>    25
<212>    DNA
<213>    Glycine max

<223>    Seq ID: 515OO2_region_G2__102179_29_Forward_Primer

<400>    1075

aatctcgatt gtcttcttgc gaaat                                    25


<210>    1076
<211>    26
<212>    DNA
<213>    Glycine max

<223>    Seq ID: 515OO2_region_G2__102179_29_Reverse_Primer

<400>    1076

tccaacaagt caacaatcaa gcaata                                   26


<210>    1077
<211>    25
<212>    DNA
<213>    Glycine max
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<223>   Seq ID: 515002_region_G2__2646_15_Forward_Primer

<400>   1077

ccaaaggctt agtttcattt gcatt   25

<210>   1078
<211>   26
<212>   DNA
<213>   Glycine max

<223>   Seq ID: 515002_region_G2__2646_15_Reverse_Primer

<400>   1078

gaaataaaca aatccaactt ctctcg   26

<210>   1079
<211>   25
<212>   DNA
<213>   Glycine max

<223>   Seq ID: 515002_region_G2__76652_24_Forward_Primer

<400>   1079

actaactctt gcgtgctcct tgttt   25

<210>   1080
<211>   24
<212>   DNA
<213>   Glycine max

<223>   Seq ID: 515002_region_G2__76652_24_Reverse_Primer

<400>   1080

ccctgggaca tatactggat caaa   24

<210>   1081
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<212>   DNA
<213>   Glycine max

<223>   Seq ID: 515002_region_G2__66280_14_Forward_Primer

<400>   1081

gtgttagatt gattaaagtt cgctga   26

<210>   1082
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<212>   DNA

<210>   Glycine max

<223>   Seq ID: 515O02_region_G2__66280_14_Reverse_Primer

<400>   1082

agatttagcc catgattaaa gtgaaa   26

<210>   1083
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<223>   Seq ID: 515O02_region_G2__54768_13_Forward_Primer

<400>   1083

aaattaccaa tcatgtatgg agtgaga   27

<210>   1084
<211>   25
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<223>   Seq ID: 515O02_region_G2__54768_13_Reverse_Primer

<400>   1084

caggcacaat attgcaccat aactt   25

<210>   1085
<211>   25
<212>   DNA
<213>   Glycine max

<223>   Seq ID: 515O02_region_G2__62580_14_Forward_Primer

<400>   1085

aacttatgga ccgtttggaa gagat   25

<210>   1086
<211>   25
<212>   DNA
<213>   Glycine max

<223>   Seq ID: 515O02_region_G2__62580_14_Reverse_Primer

<400>   1086

aaaggaggag caaagagtga agatt   25

<210>   1087

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      <211>      25
      <212>      DNA
      <213>      Glycine max

      <223>      Seq ID: 515O02_region_G2__34598_55_Forward_Primer

      <400>      1087

aaagtctggt ctgaactgac ccatt                                            25


      <210>      1088
      <211>      27
      <212>      DNA
      <213>      Glycine max

      <223>      Seq ID: 515002_region_G2__34598_55_Reverse_Primer

      <400>      1088

ggaatggaag ttatggagca gtaatgt                                          27


      <210>      1089
      <211>      27
      <212>      DNA
      <213>      Glycine max

      <223>      Seq ID: 515O02_region_G2__77680_13_Forward_Primer

      <400>      1089

tgacatgaac tatctcaaac aatgcaa                                          27


      <210>      1090
      <211>      26
      <212>      DNA
      <213>      Glycine max

      <223>      Seq ID: 515002_region_G2__77680_13_Reverse_Primer

      <400>      1090

aacaactgtt atttacacct cccaga                                           26


      <210>      1091
      <211>      27
      <212>      DNA
      <213>      Glycine max

      <223>      Seq ID: 515002_region_G2__77693_12_Forward_Primer

      <400>      1091

tgacatgaac tatctcaaac aatgcaa                                          27
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<210>       1092
<211>       26
<212>       DNA
<213>       Glycine max

<223>       Seq ID: 515002_region_G2__77693_12_Reverse_Primer

<400>       1092

aacaactgtt atttacacct cccaga                                    26


<210>       1093
<211>       26
<212>       DNA
<213>       Glycine max

<223>       Seq ID: 515002_region_G2__97392_14_Forward_Primer

<400>       1093

tttgatgtag ttgatttatg cactcg                                    26


<210>       1094
<211>       25
<212>       DNA
<213>       Glycine max

<223>       Seq ID: 515002_region_G2__97392_14_Reverse_Primer

<400>       1094

gtgacatcag gcaacctagt ttagt                                     25


<210>       1095
<211>       26
<212>       DNA
<213>       Glycine max

<223>       Seq ID: 515002_region_G2__97359_15_Forward_Primer

<400>       1095

tttgatgtag ttgatttatg cactcg                                    26


<210>       1096
<211>       25
<212>       DNA
<213>       Glycine max

<223>       Seq ID: 515002_region_G2__97359_15_Reverse_Primer

<400>       1096
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gtgacatcag gcaacctagt ttagt   25

<210>   1097
<211>   877
<212>   PRT
<213>   Glycine max

<223>   Seq ID: 240017_region_G3

<400>   1097

Met Asp Ala Cys Gly Met Ser Ser Ser Asn Ser Lys His Val Val Asp
1   5   10   15

Gln Lys Arg Ser Thr Met Asn Met Met Ile Thr Thr Ile Leu Leu Arg
            20   25   30

Phe Trp Asp Arg Tyr Asp Met Asn Cys Asp Tyr Thr Thr Asn Ser Tyr
        35   40   45

Glu Pro Gly Thr Gln Leu Ala Pro Ser Ser Pro Arg Asp Thr Ser Val
    50   55   60

Lys Leu Gly Asp Ala Ser Ser Leu Val Val Leu Pro Ser Cys Val Arg
65   70   75   80

Pro Val Leu Cys Glu Asp Glu Gly Trp Asp Gly Val Val Val Thr Ala
            85   90   95

Ser Asn Leu Leu Ala Leu Glu Ala Phe Lys Gln Glu Leu Val Asp Pro
            100   105   110

Glu Gly Phe Leu Arg Ser Trp Asn Asp Ser Gly Tyr Gly Ala Cys Ser
        115   120   125

Gly Gly Trp Val Gly Ile Lys Cys Ala Lys Gly Gln Val Ile Val Ile
    130   135   140

Gln Leu Pro Trp Lys Gly Leu Arg Gly Arg Ile Thr Asp Lys Ile Gly
145   150   155   160

Gln Leu Gln Gly Leu Arg Lys Leu Ser Leu His Asp Asn Gln Ile Gly
                165   170   175

Gly Ser Ile Pro Ser Thr Leu Gly Leu Leu Pro Asn Leu Arg Gly Val
            180   185   190

Gln Leu Phe Asn Asn Arg Leu Thr Gly Ser Ile Pro Leu Ser Leu Gly
        195   200   205

Phe Cys Pro Leu Leu Gln Ser Leu Asp Leu Ser Asn Asn Leu Leu Thr
    210   215   220

Gly Ala Ile Pro Tyr Ser Leu Ala Asn Ser Thr Lys Leu Tyr Trp Leu
225   230   235   240

Asn Leu Ser Phe Asn Ser Phe Ser Gly Pro Leu Pro Ala Ser Leu Thr

1151

```
                    245                    250                    255

His Ser Phe Ser Leu Thr Phe Leu Ser Leu Gln Asn Asn Asn Leu Ser
            260                    265                    270

Gly Ser Leu Pro Asn Ser Trp Gly Gly Asn Ser Lys Asn Gly Phe Phe
        275                    280                    285

Arg Leu Gln Asn Leu Ile Leu Asp His Asn Phe Phe Thr Gly Asp Val
    290                    295                    300

Pro Ala Ser Leu Gly Ser Leu Arg Glu Leu Asn Glu Ile Ser Leu Ser
305                    310                    315                    320

His Asn Lys Phe Ser Gly Ala Ile Pro Asn Glu Ile Gly Thr Leu Ser
                325                    330                    335

Arg Leu Lys Thr Leu Asp Ile Ser Asn Asn Ala Leu Asn Gly Asn Leu
            340                    345                    350

Pro Ala Thr Leu Ser Asn Leu Ser Ser Leu Thr Leu Leu Asn Ala Glu
        355                    360                    365

Asn Asn Leu Leu Asp Asn Gln Ile Pro Gln Ser Leu Gly Arg Leu Arg
    370                    375                    380

Asn Leu Ser Val Leu Ile Leu Ser Arg Asn Gln Phe Ser Gly His Ile
385                    390                    395                    400

Pro Ser Ser Ile Ala Asn Ile Ser Ser Leu Arg Gln Leu Asp Leu Ser
                405                    410                    415

Leu Asn Asn Phe Ser Gly Glu Ile Pro Val Ser Phe Asp Ser Gln Arg
            420                    425                    430

Ser Leu Asn Leu Phe Asn Val Ser Tyr Asn Ser Ser Leu Ser Gly Ser Val
        435                    440                    445

Pro Pro Leu Leu Ala Lys Lys Phe Asn Ser Ser Ser Phe Val Gly Asn
    450                    455                    460

Ile Gln Leu Cys Gly Tyr Ser Pro Ser Thr Pro Cys Leu Ser Gln Ala
465                    470                    475                    480

Pro Ser Gln Gly Val Ile Ala Pro Pro Pro Glu Val Ser Lys His His
                485                    490                    495

His His Arg Lys Leu Ser Thr Lys Asp Ile Ile Leu Ile Val Ala Gly
            500                    505                    510

Val Leu Leu Val Val Leu Ile Ile Leu Cys Cys Val Leu Leu Phe Cys
        515                    520                    525

Leu Ile Arg Lys Arg Ser Thr Ser Lys Ala Gly Asn Gly Gln Ala Thr
    530                    535                    540

Glu Gly Arg Ala Ala Thr Met Arg Thr Glu Lys Gly Val Pro Pro Val
545                    550                    555                    560
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Ala Gly Gly Asp Val Glu Ala Gly Gly Glu Ala Gly Gly Lys Leu Val
             565             570             575

His Phe Asp Gly Pro Met Ala Phe Thr Ala Asp Asp Leu Leu Cys Ala
             580             585             590

Thr Ala Glu Ile Met Gly Lys Ser Thr Tyr Gly Thr Val Tyr Lys Ala
         595             600             605

Ile Leu Glu Asp Gly Ser Gln Val Ala Val Lys Arg Leu Arg Glu Lys
     610             615             620

Ile Thr Lys Gly His Arg Glu Phe Glu Ser Glu Val Ser Val Leu Gly
625             630             635             640

Lys Ile Arg His Pro Asn Val Leu Ala Leu Arg Ala Tyr Tyr Leu Gly
             645             650             655

Pro Lys Gly Glu Lys Leu Leu Val Phe Asp Tyr Met Ser Lys Gly Ser
             660             665             670

Leu Ala Ser Phe Leu His Gly Gly Gly Thr Glu Thr Phe Ile Asp Trp
         675             680             685

Pro Thr Arg Met Lys Ile Ala Gln Asp Leu Ala Arg Gly Leu Phe Cys
     690             695             700

Leu His Ser Gln Glu Asn Ile Ile His Gly Asn Leu Thr Ser Ser Asn
705             710             715             720

Val Leu Leu Asp Glu Asn Thr Asn Ala Lys Ile Ala Asp Phe Gly Leu
             725             730             735

Ser Arg Leu Met Ser Thr Ala Ala Asn Ser Asn Val Ile Ala Thr Ala
             740             745             750

Gly Ala Leu Gly Tyr Arg Ala Pro Glu Leu Ser Lys Leu Lys Lys Ala
         755             760             765

Asn Thr Lys Thr Asp Ile Tyr Ser Leu Gly Val Ile Leu Leu Glu Leu
     770             775             780

Leu Thr Arg Lys Ser Pro Gly Val Ser Met Asn Gly Leu Asp Leu Pro
785             790             795             800

Gln Trp Val Ala Ser Val Val Lys Glu Glu Trp Thr Asn Glu Val Phe
             805             810             815

Asp Ala Asp Leu Met Arg Asp Ala Ser Thr Val Gly Asp Glu Leu Leu
             820             825             830

Asn Thr Leu Lys Leu Ala Leu His Cys Val Asp Pro Ser Pro Ser Ala
         835             840             845

Arg Pro Glu Val His Gln Val Leu Gln Gln Leu Glu Glu Ile Arg Pro
     850             855             860
```

1153

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Glu Arg Ser Val Thr Ala Ser Pro Gly Asp Asp Ile Val
865                 870                 875


<210>    1098
<211>    854
<212>    PRT
<213>    Glycine max

<223>    Seq ID: 24OO17_region_G3

<400>    1098

Met Val Val Ala Val Glu Lys Thr Asn Leu Thr Ser Gln Ser Gln Cys
1                 5                   10                  15

Phe Asn Arg Val Ser Asp Lys Lys Lys Glu Arg Cys Lys Thr His Met
            20                  25                  30

Asn Asn Val Asn Pro Cys Cys Phe Leu Phe Leu Leu Cys Val Trp Ser
        35                  40                  45

Leu Val Val Leu Pro Ser Cys Val Arg Pro Val Leu Cys Glu Asp Glu
    50                  55                  60

Gly Trp Asp Gly Val Val Val Thr Ala Ser Asn Leu Leu Ala Leu Glu
65                  70                  75                  80

Ala Phe Lys Gln Glu Leu Val Asp Pro Gln Gly Phe Leu Arg Ser Trp
                85                  90                  95

Asn Asp Ser Gly Tyr Gly Ala Cys Ser Gly Gly Trp Val Gly Ile Lys
            100                 105                 110

Cys Ala Lys Gly Gln Val Ile Val Ile Gln Leu Pro Trp Lys Gly Leu
        115                 120                 125

Arg Gly Arg Ile Thr Asp Lys Ile Gly Gln Leu Gln Gly Leu Arg Lys
    130                 135                 140

Leu Ser Leu His Asp Asn Gln Ile Gly Gly Ser Ile Pro Ser Thr Leu
145                 150                 155                 160

Gly Leu Leu Pro Asn Leu Arg Gly Val Gln Leu Phe Asn Asn Arg Leu
                165                 170                 175

Thr Gly Ser Ile Pro Leu Ser Leu Gly Phe Cys Pro Leu Leu Gln Ser
            180                 185                 190

Leu Asp Leu Ser Asn Asn Leu Leu Thr Gly Ala Ile Pro Tyr Ser Leu
        195                 200                 205

Ala Asn Ser Thr Lys Leu Tyr Trp Leu Asn Leu Ser Phe Asn Ser Phe
    210                 215                 220

Ser Gly Pro Leu Pro Ala Ser Leu Thr His Ser Phe Ser Leu Thr Phe
225                 230                 235                 240
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Leu Ser Leu Gln Asn Asn Asn Leu Ser Gly Ser Leu Pro Asn Ser Trp
                245                 250                 255

Gly Gly Asn Ser Lys Asn Gly Phe Phe Arg Leu Gln Asn Leu Ile Leu
                260                 265                 270

Asp His Asn Phe Phe Thr Gly Asp Val Pro Ala Ser Leu Gly Ser Leu
            275                 280                 285

Arg Glu Leu Asn Glu Ile Ser Leu Ser His Asn Lys Phe Ser Gly Ala
    290                 295                 300

Ile Pro Asn Glu Ile Gly Thr Leu Ser Arg Leu Lys Thr Leu Asp Ile
305                 310                 315                 320

Ser Asn Asn Ala Leu Asn Gly Asn Leu Pro Ala Thr Leu Ser Asn Leu
                325                 330                 335

Ser Ser Leu Thr Leu Leu Asn Ala Glu Asn Asn Leu Leu Asp Asn Gln
                340                 345                 350

Ile Pro Gln Ser Leu Gly Arg Leu Arg Asn Leu Ser Val Leu Ile Leu
            355                 360                 365

Ser Arg Asn Gln Phe Ser Gly His Ile Pro Ser Ser Ile Ala Asn Ile
    370                 375                 380

Ser Ser Leu Arg Gln Leu Asp Leu Ser Leu Asn Asn Phe Ser Gly Glu
385                 390                 395                 400

Ile Pro Val Ser Phe Asp Ser Gln Arg Ser Leu Asn Leu Phe Asn Val
            405                 410                 415

Ser Tyr Asn Ser Leu Ser Gly Ser Val Pro Pro Leu Leu Ala Lys Lys
            420                 425                 430

Phe Asn Ser Ser Ser Phe Val Gly Asn Ile Gln Leu Cys Gly Tyr Ser
            435                 440                 445

Pro Ser Thr Pro Cys Leu Ser Gln Ala Pro Ser Gln Gly Val Ile Ala
    450                 455                 460

Pro Pro Pro Glu Val Ser Lys His His His His Arg Lys Leu Ser Thr
465                 470                 475                 480

Lys Asp Ile Ile Leu Ile Val Ala Gly Val Leu Leu Val Val Leu Ile
            485                 490                 495

Ile Leu Cys Cys Val Leu Leu Phe Cys Leu Ile Arg Lys Arg Ser Thr
            500                 505                 510

Ser Lys Ala Gly Asn Gly Gln Ala Thr Glu Gly Arg Ala Ala Thr Met
            515                 520                 525

Arg Thr Glu Lys Gly Val Pro Pro Val Ala Gly Gly Asp Val Glu Ala
    530                 535                 540

Gly Gly Glu Ala Gly Gly Lys Leu Val His Phe Asp Gly Pro Met Ala
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    545              550              555              560

Phe Thr Ala Asp Asp Leu Leu Cys Ala Thr Ala Glu Ile Met Gly Lys
             565                        570                575

Ser Thr Tyr Gly Thr Val Tyr Lys Ala Ile Leu Glu Asp Gly Ser Gln
         580                    585                    590

Val Ala Val Lys Arg Leu Arg Glu Lys Ile Thr Lys Gly His Arg Glu
         595                    600                    605

Phe Glu Ser Glu Val Ser Val Leu Gly Lys Ile Arg His Pro Asn Val
    610                    615                    620

Leu Ala Leu Arg Ala Tyr Tyr Leu Gly Pro Lys Gly Glu Lys Leu Leu
625                    630                    635                640

Val Phe Asp Tyr Met Ser Lys Gly Ser Leu Ala Ser Phe Leu His Gly
             645                    650                    655

Gly Gly Thr Glu Thr Phe Ile Asp Trp Pro Thr Arg Met Lys Ile Ala
             660                    665                    670

Gln Asp Leu Ala Arg Gly Leu Phe Cys Leu His Ser Gln Glu Asn Ile
         675                    680                    685

Ile His Gly Asn Leu Thr Ser Ser Asn Val Leu Leu Asp Glu Asn Thr
    690                    695                    700

Asn Ala Lys Ile Ala Asp Phe Gly Leu Ser Arg Leu Met Ser Thr Ala
705                    710                    715                720

Ala Asn Ser Asn Val Ile Ala Thr Ala Gly Ala Leu Gly Tyr Arg Ala
             725                    730                    735

Pro Glu Leu Ser Lys Leu Lys Lys Ala Asn Thr Lys Thr Asp Ile Tyr
             740                    745                    750

Ser Leu Gly Val Ile Leu Leu Glu Leu Leu Thr Arg Lys Ser Pro Gly
         755                    760                    765

Val Ser Met Asn Gly Leu Asp Leu Pro Gln Trp Val Ala Ser Val Val
    770                    775                    780

Lys Glu Glu Trp Thr Asn Glu Val Phe Asp Ala Asp Leu Met Arg Asp
785                    790                    795                800

Ala Ser Thr Val Gly Asp Glu Leu Leu Asn Thr Leu Lys Leu Ala Leu
             805                    810                    815

His Cys Val Asp Pro Ser Pro Ser Ala Arg Pro Glu Val His Gln Val
             820                    825                    830

Leu Gln Gln Leu Glu Glu Ile Arg Pro Glu Arg Ser Val Thr Ala Ser
         835                    840                    845

Pro Gly Asp Asp Ile Val
    850
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<210>      1099
<211>      894
<212>      PRT
<213>      Glycine max

<223>      Seq ID: 318O13_region_A3

<400>      1099

Met Ser Asn Phe Leu Lys Ser Leu Thr Pro Pro Pro Ser Gly Trp Ser
1                5                  10                  15

Glu Thr Thr Pro Phe Cys Gln Trp Lys Gly Ile Gln Cys Asp Ser Ser
            20                  25                  30

Ser His Val Thr Ser Ile Ser Leu Ala Ser His Ser Leu Thr Gly Thr
        35                  40                  45

Leu Pro Ser Asp Leu Asn Ser Leu Ser Gln Leu Arg Thr Leu Ser Leu
    50                  55                  60

Gln Asp Asn Ser Leu Thr Gly Thr Leu Pro Ser Leu Ser Asn Leu Ser
65                  70                  75                  80

Phe Leu Gln Thr Val Tyr Leu Asn Arg Asn Asn Phe Ser Ser Val Ser
                85                  90                  95

Pro Thr Ala Phe Ala Ser Leu Thr Ser Leu Gln Thr Leu Ser Leu Gly
            100                 105                 110

Ser Asn Pro Ala Leu Gln Pro Trp Ser Phe Pro Thr Asp Leu Thr Ser
        115                 120                 125

Ser Ser Asn Leu Ile Asp Leu Asp Leu Ala Thr Val Ser Leu Thr Gly
    130                 135                 140

Pro Leu Pro Asp Ile Phe Asp Lys Phe Pro Ser Leu Gln His Leu Arg
145                 150                 155                 160

Leu Ser Tyr Asn Asn Leu Thr Gly Asn Leu Pro Ser Ser Phe Ser Ala
                165                 170                 175

Ala Asn Asn Leu Glu Thr Leu Trp Leu Asn Asn Gln Ala Ala Gly Leu
            180                 185                 190

Ser Gly Thr Leu Leu Val Leu Ser Asn Met Ser Ala Leu Asn Gln Ser
        195                 200                 205

Trp Leu Asn Lys Asn Gln Phe Thr Gly Ser Ile Pro Asp Leu Ser Gln
    210                 215                 220

Cys Thr Ala Leu Ser Asp Leu Gln Leu Arg Asp Asn Gln Leu Thr Gly
225                 230                 235                 240

Val Val Pro Ala Ser Leu Thr Ser Pro Ser Leu Lys Lys Val Ser
                245                 250                 255
```

```
Leu Asp Asn Asn Glu Leu Gln Gly Pro Val Pro Val Phe Gly Lys Gly
            260               265               270

Val Asn Val Thr Leu Asp Gly Ile Asn Ser Phe Cys Leu Asp Thr Pro
            275               280               285

Gly Asn Cys Asp Pro Arg Val Met Val Leu Leu Gln Ile Ala Glu Ala
    290               295               300

Phe Gly Tyr Pro Ile Arg Leu Ala Glu Ser Trp Lys Gly Asn Asp Pro
305               310               315               320

Cys Asp Gly Trp Asn Tyr Val Val Cys Ala Ala Gly Lys Ile Ile Thr
            325               330               335

Val Asn Phe Glu Lys Gln Gly Leu Gln Gly Thr Ile Ser Pro Ala Phe
            340               345               350

Ala Asn Leu Thr Asp Leu Arg Thr Leu Phe Leu Asn Gly Asn Asn Leu
            355               360               365

Ile Gly Ser Ile Pro Asp Ser Leu Ile Thr Leu Pro Gln Leu Gln Thr
    370               375               380

Leu Asp Val Ser Asp Asn Asn Leu Ser Gly Leu Val Pro Lys Phe Pro
385               390               395               400

Pro Lys Val Lys Leu Val Thr Ala Gly Asn Ala Leu Leu Gly Lys Pro
            405               410               415

Leu Ser Pro Gly Gly Gly Pro Ser Gly Thr Thr Pro Ser Gly Ser Ser
            420               425               430

Thr Gly Gly Ser Gly Gly Glu Ser Ser Lys Gly Asn Ser Ser Val Ser
            435               440               445

Pro Gly Trp Ile Ala Gly Ile Val Val Ile Val Leu Phe Phe Ile Ala
    450               455               460

Val Val Leu Phe Val Ser Trp Lys Cys Phe Val Asn Lys Leu Gln Gly
465               470               475               480

Lys Phe Ser Arg Val Lys Gly His Glu Asn Gly Lys Gly Gly Phe Lys
            485               490               495

Leu Asp Ala Val His Val Ser Asn Gly Tyr Gly Gly Val Pro Val Glu
            500               505               510

Leu Gln Ser Gln Ser Ser Gly Asp Arg Ser Asp Leu His Ala Leu Asp
            515               520               525

Gly Pro Thr Phe Ser Ile Gln Val Leu Arg Gln Val Thr Asn Asn Phe
    530               535               540

Ser Glu Glu Asn Ile Leu Gly Arg Gly Gly Phe Gly Val Val Tyr Lys
545               550               555               560
```

1158

Gly Val Leu His Asp Gly Thr Lys Ile Ala Val Lys Arg Met Glu Ser
                565   570   575

Val Ala Met Gly Asn Lys Gly Gln Lys Glu Phe Glu Ala Glu Ile Ala
            580   585   590

Leu Leu Ser Lys Val Arg His Arg His Leu Val Ala Leu Leu Gly Tyr
        595   600   605

Cys Ile Asn Gly Asn Glu Arg Leu Leu Val Tyr Glu Tyr Met Pro Gln
    610   615   620

Gly Thr Leu Thr Gln His Leu Phe Glu Trp Gln Glu His Gly Tyr Ala
625   630   635   640

Pro Leu Thr Trp Lys Gln Arg Val Val Ile Ala Leu Asp Val Ala Arg
                645   650   655

Gly Val Glu Tyr Leu His Ser Leu Ala Gln Gln Ser Phe Ile His Arg
            660   665   670

Asp Leu Lys Pro Ser Asn Ile Leu Leu Gly Asp Asp Met Arg Ala Lys
        675   680   685

Val Ala Asp Phe Gly Leu Val Lys Asn Ala Pro Asp Gly Lys Tyr Ser
    690   695   700

Val Glu Thr Arg Leu Ala Gly Thr Phe Gly Tyr Leu Ala Pro Glu Tyr
705   710   715   720

Ala Ala Thr Gly Arg Val Thr Thr Lys Val Asp Val Tyr Ala Phe Gly
                725   730   735

Val Val Leu Met Glu Leu Ile Thr Gly Arg Lys Ala Leu Asp Asp Thr
            740   745   750

Val Pro Asp Glu Arg Ser His Leu Val Thr Trp Phe Arg Arg Val Leu
        755   760   765

Ile Asn Lys Glu Asn Ile Pro Lys Ala Ile Asp Gln Ile Leu Asn Pro
    770   775   780

Asp Glu Glu Thr Met Gly Ser Ile Tyr Thr Val Ala Glu Leu Ala Gly
785   790   795   800

His Cys Thr Ala Arg Glu Pro Tyr Gln Arg Pro Asp Met Gly His Ala
                805   810   815

Val Asn Val Leu Val Pro Leu Val Glu Gln Trp Lys Pro Thr Ser His
            820   825   830

Asp Glu Glu Glu Asp Gly Ser Gly Gly Asp Leu His Met Ser Leu
        835   840   845

Pro Gln Ala Leu Arg Arg Trp Gln Ala Asn Glu Gly Thr Ser Ser Ile
    850   855   860

Phe Asn Asp Ile Ser Ile Ser Gln Thr Gln Ser Ser Ile Ser Ser Lys

```
865              870                875              880

Pro Ala Gly Phe Ala Asp Ser Phe Asp Ser Met Asp Cys Arg
                 885                 890


<210>    1100
<211>    877
<212>    PRT
<213>    Glycine max

<223>    Seq ID: rhg1_A3244_amplicon

<400>    1100

Met Asp Ala Cys Gly Met Ser Ser Ser Asn Ser Lys His Val Val Asp
1               5               10                  15

Gln Lys Arg Ser Thr Met Asn Met Met Ile Thr Thr Ile Leu Leu Arg
            20              25              30

Phe Trp Asp Arg Tyr Asp Met Asn Cys Asp Tyr Thr Thr Asn Ser Tyr
         35              40              45

Glu Pro Gly Thr Gln Leu Ala Pro Ser Ser Pro Arg Asp Thr Ser Val
    50              55              60

Lys Leu Gly Asp Ala Ser Ser Leu Val Val Leu Pro Ser Cys Val Arg
65              70              75              80

Pro Val Leu Cys Glu Asp Glu Gly Trp Asp Gly Val Val Val Thr Ala
             85              90              95

Ser Asn Leu Leu Ala Leu Glu Ala Phe Lys Gln Glu Leu Val Asp Pro
         100             105             110

Glu Gly Phe Leu Arg Ser Trp Asn Asp Ser Gly Tyr Gly Ala Cys Ser
        115             120             125

Gly Gly Trp Val Gly Ile Lys Cys Ala Lys Gly Gln Val Ile Val Ile
130             135             140

Gln Leu Pro Trp Lys Gly Leu Arg Gly Arg Ile Thr Asp Lys Ile Gly
145             150             155             160

Gln Leu Gln Gly Leu Arg Lys Leu Ser Leu His Asp Asn Gln Ile Gly
            165             170             175

Gly Ser Ile Pro Ser Thr Leu Gly Leu Leu Pro Asn Leu Arg Gly Val
        180             185             190

Gln Leu Phe Asn Asn Arg Leu Thr Gly Ser Ile Pro Leu Ser Leu Gly
        195             200             205

Phe Cys Pro Leu Leu Gln Ser Leu Asp Leu Ser Asn Asn Leu Leu Thr
    210             215             220

Gly Ala Ile Pro Tyr Ser Leu Ala Asn Ser Thr Lys Leu Tyr Trp Leu
```

```
        225                 230                 235                 240

    Asn Leu Ser Phe Asn Ser Phe Ser Gly Pro Leu Pro Ala Ser Leu Thr
                    245                 250                 255

    His Ser Phe Ser Leu Thr Phe Leu Ser Leu Gln Asn Asn Asn Leu Ser
                260                 265                 270

    Gly Ser Leu Pro Asn Ser Trp Gly Gly Asn Ser Lys Asn Gly Phe Phe
            275                 280                 285

    Arg Leu Gln Asn Leu Ile Leu Asp His Asn Phe Phe Thr Gly Asp Val
        290                 295                 300

    Pro Ala Ser Leu Gly Ser Leu Arg Glu Leu Asn Glu Ile Ser Leu Ser
    305                 310                 315                 320

    His Asn Lys Phe Ser Gly Ala Ile Pro Asn Glu Ile Gly Thr Leu Ser
                    325                 330                 335

    Arg Leu Lys Thr Leu Asp Ile Ser Asn Asn Ala Leu Asn Gly Asn Leu
                340                 345                 350

    Pro Ala Thr Leu Ser Asn Leu Ser Ser Leu Thr Leu Leu Asn Ala Glu
                355                 360                 365

    Asn Asn Leu Leu Asp Asn Gln Ile Pro Gln Ser Leu Gly Arg Leu Arg
        370                 375                 380

    Asn Leu Ser Val Leu Ile Leu Ser Arg Asn Gln Phe Ser Gly His Ile
    385                 390                 395                 400

    Pro Ser Ser Ile Ala Asn Ile Ser Ser Leu Arg Gln Leu Asp Leu Ser
                    405                 410                 415

    Leu Asn Asn Phe Ser Gly Glu Ile Pro Val Ser Phe Asp Ser Gln Arg
                420                 425                 430

    Ser Leu Asn Leu Phe Asn Val Ser Tyr Asn Ser Leu Ser Gly Ser Val
            435                 440                 445

    Pro Pro Leu Leu Ala Lys Lys Phe Asn Ser Ser Ser Phe Val Gly Asn
        450                 455                 460

    Ile Gln Leu Cys Gly Tyr Ser Pro Ser Thr Pro Cys Leu Ser Gln Ala
    465                 470                 475                 480

    Pro Ser Gln Gly Val Ile Ala Pro Pro Pro Glu Val Ser Lys His His
                485                 490                 495

    His His Arg Lys Leu Ser Thr Lys Asp Ile Ile Leu Ile Val Ala Gly
                500                 505                 510

    Val Leu Leu Val Val Leu Ile Ile Leu Cys Cys Val Leu Leu Phe Cys
            515                 520                 525

    Leu Ile Arg Lys Arg Ser Thr Ser Lys Ala Gly Asn Gly Gln Ala Thr
        530                 535                 540
```

```
Glu Gly Arg Ala Ala Thr Met Arg Thr Glu Lys Gly Val Pro Pro Val
545                 550                 555                 560

Ala Gly Gly Asp Val Glu Ala Gly Gly Glu Ala Gly Gly Lys Leu Val
                565                 570                 575

His Phe Asp Gly Pro Met Ala Phe Thr Ala Asp Asp Leu Leu Cys Ala
            580                 585                 590

Thr Ala Glu Ile Met Gly Lys Ser Thr Tyr Gly Thr Val Tyr Lys Ala
        595                 600                 605

Ile Leu Glu Asp Gly Ser Gln Val Ala Val Lys Arg Leu Arg Glu Lys
    610                 615                 620

Ile Thr Lys Gly His Arg Glu Phe Glu Ser Glu Val Ser Val Leu Gly
625                 630                 635                 640

Lys Ile Arg His Pro Asn Val Leu Ala Leu Arg Ala Tyr Tyr Leu Gly
                645                 650                 655

Pro Lys Gly Glu Lys Leu Leu Val Phe Asp Tyr Met Ser Lys Gly Ser
            660                 665                 670

Leu Ala Ser Phe Leu His Gly Gly Gly Thr Glu Thr Phe Ile Asp Trp
        675                 680                 685

Pro Thr Arg Met Lys Ile Ala Gln Asp Leu Ala Arg Gly Leu Phe Cys
    690                 695                 700

Leu His Ser Gln Glu Asn Ile Ile His Gly Asn Leu Thr Ser Ser Asn
705                 710                 715                 720

Val Leu Leu Asp Glu Asn Thr Asn Ala Lys Ile Ala Asp Phe Gly Leu
                725                 730                 735

Ser Arg Leu Met Ser Thr Ala Ala Asn Ser Asn Val Ile Ala Thr Ala
            740                 745                 750

Gly Ala Leu Gly Tyr Arg Ala Pro Glu Leu Ser Lys Leu Lys Lys Ala
        755                 760                 765

Asn Thr Lys Thr Asp Ile Tyr Ser Leu Gly Val Ile Leu Leu Glu Leu
    770                 775                 780

Leu Thr Arg Lys Ser Pro Gly Val Ser Met Asn Gly Leu Asp Leu Pro
785                 790                 795                 800

Gln Trp Val Ala Ser Val Val Lys Glu Glu Trp Thr Asn Glu Val Phe
                805                 810                 815

Asp Ala Asp Leu Met Arg Asp Ala Ser Thr Val Gly Asp Glu Leu Leu
            820                 825                 830

Asn Thr Leu Lys Leu Ala Leu His Cys Val Asp Pro Ser Pro Ser Ala
        835                 840                 845
```

Arg Pro Glu Val His Gln Val Leu Gln Gln Leu Glu Glu Ile Arg Pro
    850   855   860

Glu Arg Ser Val Thr Ala Ser Pro Gly Asp Asp Ile Val
865   870   875

<210>   1101
<211>   854
<212>   PRT
<213>   Glycine max

<223>   Seq ID: rhg1_A3244_amplicon

<400>   1101

Met Val Val Ala Val Glu Lys Thr Asn Leu Thr Ser Gln Ser Gln Cys
1   5   10   15

Phe Asn Arg Val Ser Asp Lys Lys Lys Glu Arg Cys Lys Thr His Met
            20   25   30

Asn Asn Val Asn Pro Cys Cys Phe Leu Phe Leu Leu Cys Val Trp Ser
        35   40   45

Leu Val Val Leu Pro Ser Cys Val Arg Pro Val Leu Cys Glu Asp Glu
    50   55   60

Gly Trp Asp Gly Val Val Val Thr Ala Ser Asn Leu Leu Ala Leu Glu
65   70   75   80

Ala Phe Lys Gln Glu Leu Val Asp Pro Glu Gly Phe Leu Arg Ser Trp
                85   90   95

Asn Asp Ser Gly Tyr Gly Ala Cys Ser Gly Gly Trp Val Gly Ile Lys
            100   105   110

Cys Ala Lys Gly Gln Val Ile Val Ile Gln Leu Pro Trp Lys Gly Leu
        115   120   125

Arg Gly Arg Ile Thr Asp Lys Ile Gly Gln Leu Gln Gly Leu Arg Lys
    130   135   140

Leu Ser Leu His Asp Asn Gln Ile Gly Gly Ser Ile Pro Ser Thr Leu
145   150   155   160

Gly Leu Leu Pro Asn Leu Arg Gly Val Gln Leu Phe Asn Asn Arg Leu
                165   170   175

Thr Gly Ser Ile Pro Leu Ser Leu Gly Phe Cys Pro Leu Leu Gln Ser
            180   185   190

Leu Asp Leu Ser Asn Asn Leu Leu Thr Gly Ala Ile Pro Tyr Ser Leu
    195   200   205

Ala Asn Ser Thr Lys Leu Tyr Trp Leu Asn Leu Ser Phe Asn Ser Phe
    210   215   220

Ser Gly Pro Leu Pro Ala Ser Leu Thr His Ser Phe Ser Leu Thr Phe
225   230   235   240

Leu Ser Leu Gln Asn Asn Asn Leu Ser Gly Ser Leu Pro Asn Ser Trp
                245   250   255

Gly Gly Asn Ser Lys Asn Gly Phe Phe Arg Leu Gln Asn Leu Ile Leu
                260   265   270

Asp His Asn Phe Phe Thr Gly Asp Val Pro Ala Ser Leu Gly Ser Leu
            275   280   285

Arg Glu Leu Asn Glu Ile Ser Leu Ser His Asn Lys Phe Ser Gly Ala
        290   295   300

Ile Pro Asn Glu Ile Gly Thr Leu Ser Arg Leu Lys Thr Leu Asp Ile
305   310   315   320

Ser Asn Asn Ala Leu Asn Gly Asn Leu Pro Ala Thr Leu Ser Asn Leu
                325   330   335

Ser Ser Leu Thr Leu Leu Asn Ala Glu Asn Asn Leu Leu Asp Asn Gln
            340   345   350

Ile Pro Gln Ser Leu Gly Arg Leu Arg Asn Leu Ser Val Leu Ile Leu
            355   360   365

Ser Arg Asn Gln Phe Ser Gly His Ile Pro Ser Ser Ile Ala Asn Ile
        370   375   380

Ser Ser Leu Arg Gln Leu Asp Leu Ser Leu Asn Asn Phe Ser Gly Glu
385   390   395   400

Ile Pro Val Ser Phe Asp Ser Gln Arg Ser Leu Asn Leu Phe Asn Val
                405   410   415

Ser Tyr Asn Ser Leu Ser Gly Ser Val Pro Pro Leu Leu Ala Lys Lys
            420   425   430

Phe Asn Ser Ser Ser Phe Val Gly Asn Ile Gln Leu Cys Gly Tyr Ser
            435   440   445

Pro Ser Thr Pro Cys Leu Ser Gln Ala Pro Pro Ser Gln Gly Val Ile Ala
        450   455   460

Pro Pro Pro Glu Val Ser Lys His His His His Arg Lys Leu Ser Thr
465   470   475   480

Lys Asp Ile Ile Leu Ile Val Ala Gly Val Leu Leu Val Val Leu Ile
            485   490   495

Ile Leu Cys Cys Val Leu Leu Phe Cys Leu Ile Arg Lys Arg Ser Thr
            500   505   510

Ser Lys Ala Gly Asn Gly Gln Ala Thr Glu Gly Arg Ala Ala Thr Met
        515   520   525

Arg Thr Glu Lys Gly Val Pro Pro Val Ala Gly Gly Asp Val Glu Ala

```
        530                    535                    540

Gly Gly Glu Ala Gly Gly Lys Leu Val His Phe Asp Gly Pro Met Ala
545                 550                    555                    560

Phe Thr Ala Asp Asp Leu Leu Cys Ala Thr Ala Glu Ile Met Gly Lys
                565                    570                    575

Ser Thr Tyr Gly Thr Val Tyr Lys Ala Ile Leu Glu Asp Gly Ser Gln
            580                    585                    590

Val Ala Val Lys Arg Leu Arg Glu Lys Ile Thr Lys Gly His Arg Glu
            595                    600                    605

Phe Glu Ser Glu Val Ser Val Leu Gly Lys Ile Arg His Pro Asn Val
    610                    615                    620

Leu Ala Leu Arg Ala Tyr Tyr Leu Gly Pro Lys Gly Glu Lys Leu Leu
625                 630                    635                    640

Val Phe Asp Tyr Met Ser Lys Gly Ser Leu Ala Ser Phe Leu His Gly
                645                    650                    655

Gly Gly Thr Glu Thr Phe Ile Asp Trp Pro Thr Arg Met Lys Ile Ala
            660                    665                    670

Gln Asp Leu Ala Arg Gly Leu Phe Cys Leu His Ser Gln Glu Asn Ile
    675                    680                    685

Ile His Gly Asn Leu Thr Ser Ser Asn Val Leu Leu Asp Glu Asn Thr
    690                    695                    700

Asn Ala Lys Ile Ala Asp Phe Gly Leu Ser Arg Leu Met Ser Thr Ala
705                 710                    715                    720

Ala Asn Ser Asn Val Ile Ala Thr Ala Gly Ala Leu Gly Tyr Arg Ala
                725                    730                    735

Pro Glu Leu Ser Lys Leu Lys Lys Ala Asn Thr Lys Thr Asp Ile Tyr
            740                    745                    750

Ser Leu Gly Val Ile Leu Leu Glu Leu Leu Thr Arg Lys Ser Pro Gly
            755                    760                    765

Val Ser Met Asn Gly Leu Asp Leu Pro Gln Trp Val Ala Ser Val Val
    770                    775                    780

Lys Glu Glu Trp Thr Asn Glu Val Phe Asp Ala Asp Leu Met Arg Asp
785                 790                    795                    800

Ala Ser Thr Val Gly Asp Glu Leu Leu Asn Thr Leu Lys Leu Ala Leu
                805                    810                    815

His Cys Val Asp Pro Ser Pro Ser Ala Arg Pro Glu Val His Gln Val
            820                    825                    830

Leu Gln Gln Leu Glu Glu Ile Arg Pro Glu Arg Ser Val Thr Ala Ser
            835                    840                    845
```

```
Pro Gly Asp Asp Ile Val
    850


<210>     1102
<211>     877
<212>     PRT
<213>     Glycine max

<223>     Seq ID: rhg1_peking_amplicon

<400>     1102

Met Asp Ala Cys Gly Met Ser Ser Ser Asn Ser Lys His Val Val Asp
1                   5                   10                  15

Gln Lys Arg Ser Thr Met Asn Met Met Ile Thr Thr Ile Leu Leu Arg
            20                  25                  30

Phe Trp Asp Arg Tyr Asp Met Asn Cys Asp Tyr Thr Thr Asn Ser Tyr
        35                  40                  45

Glu Pro Gly Thr Gln Leu Ala Pro Ser Ser Pro Arg Asp Thr Ser Val
    50                  55                  60

Lys Leu Gly Asp Ala Ser Ser Leu Val Val Leu Pro Ser Cys Val Arg
65                  70                  75                  80

Pro Val Leu Cys Glu Asp Glu Gly Trp Asp Gly Val Val Val Thr Ala
                85                  90                  95

Ser Asn Leu Leu Ala Leu Glu Ala Phe Lys Gln Glu Leu Ala Asp Pro
            100                 .    105                 110

Glu Gly Phe Leu Arg Ser Trp Asn Asp Ser Gly Tyr Gly Ala Cys Ser
        115                 120                 125

Gly Gly Trp Val Gly Ile Lys Cys Ala Gln Gly Gln Val Ile Val Ile
    130                 135                 140

Gln Leu Pro Trp Lys Gly Leu Arg Gly Arg Ile Thr Asp Lys Ile Gly
145                 150                 155                 160

Gln Leu Gln Leu Arg Lys Leu Ser Ser Leu His Asp Asn Gln Ile Gly
            165                 170                 175

Gly Ser Ile Pro Ser Thr Leu Gly Leu Leu Pro Asn Leu Arg Gly Val
            180                 185                 190

Gln Leu Phe Asn Asn Arg Leu Thr Gly Ser Ile Pro Leu Ser Leu Gly
        195                 200                 205

Phe Cys Pro Leu Leu Gln Ser Leu Asp Leu Ser Asn Asn Leu Leu Thr
    210                 215                 220

Gly Ala Ile Pro Tyr Ser Leu Ala Asn Ser Thr Lys Leu Tyr Trp Leu
225                 230                 235                 240
```

```
Asn Leu Ser Phe Asn Ser Phe Ser Gly Pro Leu Pro Ala Ser Leu Thr
                245                 250                 255

His Ser Phe Ser Leu Thr Phe Leu Ser Leu Gln Asn Asn Asn Leu Ser
                260                 265                 270

Gly Ser Leu Pro Asn Ser Trp Gly Gly Asn Ser Lys Asn Gly Phe Phe
            275                 280                 285

Arg Leu Gln Asn Leu Ile Leu Asp His Asn Phe Phe Thr Gly Asp Val
        290                 295                 300

Pro Ala Ser Leu Gly Ser Leu Arg Glu Leu Asn Glu Ile Ser Leu Ser
305                 310                 315                 320

His Asn Lys Phe Ser Gly Ala Ile Pro Asn Glu Ile Gly Thr Leu Ser
                325                 330                 335

Arg Leu Lys Thr Leu Asp Ile Ser Asn Ala Leu Asn Gly Asn Leu
            340                 345                 350

Pro Ala Thr Leu Ser Asn Leu Ser Ser Leu Thr Leu Leu Asn Ala Glu
            355                 360                 365

Asn Asn Leu Leu Asp Asn Gln Ile Pro Gln Ser Leu Gly Arg Leu Arg
        370                 375                 380

Asn Leu Ser Val Leu Ile Leu Ser Arg Asn Gln Phe Ser Gly His Ile
385                 390                 395                 400

Pro Ser Ser Ile Ala Asn Ile Ser Ser Leu Arg Gln Leu Asp Leu Ser
                405                 410                 415

Leu Asn Asn Phe Ser Gly Glu Ile Pro Val Ser Phe Asp Ser Gln Arg
            420                 425                 430

Ser Leu Asn Leu Phe Asn Val Ser Tyr Asn Ser Leu Ser Gly Ser Val
            435                 440                 445

Pro Pro Leu Leu Ala Lys Lys Phe Asn Ser Ser Ser Phe Val Gly Asn
    450                 455                 460

Ile Gln Leu Cys Gly Tyr Ser Pro Ser Thr Pro Cys Leu Ser Gln Ala
465                 470                 475                 480

Pro Ser Gln Gly Val Ile Ala Pro Pro Glu Val Ser Lys His His
            485                 490                 495

His His Arg Lys Leu Ser Thr Lys Asp Ile Ile Leu Ile Val Ala Gly
        500                 505                 510

Val Leu Leu Val Val Leu Ile Ile Leu Cys Cys Val Leu Leu Phe Cys
        515                 520                 525

Leu Ile Arg Lys Arg Ser Thr Ser Lys Ala Gly Asn Gly Gln Ala Thr
    530                 535                 540
```

```
Glu Gly Arg Ala Ala Thr Met Arg Thr Glu Lys Gly Val Pro Pro Val
545                 550                 555                 560

Ala Gly Gly Asp Val Glu Ala Gly Gly Glu Ala Gly Gly Lys Leu Val
                565                 570                 575

His Phe Asp Gly Pro Met Ala Phe Thr Ala Asp Asp Leu Leu Cys Ala
            580                 585                 590

Thr Ala Glu Ile Met Gly Lys Ser Thr Tyr Gly Thr Val Tyr Lys Ala
        595                 600                 605

Ile Leu Glu Asp Gly Ser Gln Val Ala Val Lys Arg Leu Arg Glu Lys
    610                 615                 620

Ile Thr Lys Gly His Arg Glu Phe Glu Ser Glu Val Ser Val Leu Gly
625                 630                 635                 640

Lys Ile Arg His Pro Asn Val Leu Ala Leu Arg Ala Tyr Tyr Leu Gly
            645                 650                 655

Pro Lys Gly Glu Lys Leu Leu Val Phe Asp Tyr Met Ser Lys Gly Ser
        660                 665                 670

Leu Ala Ser Phe Leu His Gly Gly Thr Glu Thr Phe Ile Asp Trp
        675                 680                 685

Pro Thr Arg Met Lys Ile Ala Gln Asp Leu Ala Arg Gly Leu Phe Cys
    690                 695                 700

Leu His Ser Gln Glu Asn Ile Ile His Gly Asn Leu Thr Ser Ser Asn
705                 710                 715                 720

Val Leu Leu Asp Glu Asn Thr Asn Ala Lys Ile Ala Asp Phe Gly Leu
                725                 730                 735

Ser Arg Leu Met Ser Thr Ala Ala Asn Ser Asn Val Ile Ala Thr Ala
            740                 745                 750

Gly Ala Leu Gly Tyr Arg Ala Pro Glu Leu Ser Lys Leu Lys Lys Ala
        755                 760                 765

Asn Thr Lys Thr Asp Ile Tyr Ser Leu Gly Val Ile Leu Leu Glu Leu
    770                 775                 780

Leu Thr Arg Lys Ser Pro Gly Val Ser Met Asn Gly Leu Asp Leu Pro
785                 790                 795                 800

Gln Trp Val Ala Ser Val Val Lys Glu Glu Trp Thr Asn Glu Val Phe
                805                 810                 815

Asp Ala Asp Leu Met Arg Asp Ala Ser Thr Val Gly Asp Glu Leu Leu
            820                 825                 830

Asn Thr Leu Lys Leu Ala Leu His Cys Val Asp Pro Ser Pro Ser Ala
        835                 840                 845

Arg Pro Glu Val His Gln Val Leu Gln Gln Leu Glu Glu Ile Arg Pro
```

1168

```
        850                    855                    860

Glu Arg Ser Val Thr Ala Ser Pro Gly Asp Asp Ile Val
865                    870                    875



<210>      1103
<211>      854
<212>      PRT
<213>      Glycine max

<223>      Seq ID: rhg1_peking_amplicon

<400>      1103

Met Val Val Ala Val Glu Lys Thr Asn Leu Thr Ser Gln Ser Gln Cys
1                   5                    10                   15

Phe Asn Arg Val Ser Asp Lys Lys Lys Glu Arg Cys Lys Thr His Met
                20                   25                   30

Asn Asn Val Asn Pro Cys Cys Phe Leu Phe Leu Leu Cys Val Trp Ser
        35                   40                   45

Leu Val Val Leu Pro Ser Cys Val Arg Pro Val Leu Cys Glu Asp Glu
    50                   55                   60

Gly Trp Asp Gly Val Val Val Thr Ala Ser Asn Leu Leu Ala Leu Glu
65                   70                   75                   80

Ala Phe Lys Gln Glu Leu Ala Asp Pro Glu Gly Phe Leu Arg Ser Trp
                85                   90                   95

Asn Asp Ser Gly Tyr Gly Ala Cys Ser Gly Gly Trp Val Gly Ile Lys
            100                  105                  110

Cys Ala Gln Gly Gln Val Ile Val Ile Gln Leu Pro Trp Lys Gly Leu
        115                  120                  125

Arg Gly Arg Ile Thr Asp Lys Ile Gly Gln Leu Gln Gly Leu Arg Lys
    130                  135                  140

Leu Ser Leu His Asp Asn Gln Ile Gly Gly Ser Ile Pro Ser Thr Leu
145                  150                  155                  160

Gly Leu Leu Pro Asn Leu Arg Gly Val Gln Leu Phe Asn Asn Arg Leu
                165                  170                  175

Thr Gly Ser Ile Pro Leu Ser Leu Gly Phe Cys Pro Leu Leu Gln Ser
            180                  185                  190

Leu Asp Leu Ser Asn Asn Leu Leu Thr Gly Ala Ile Pro Tyr Ser Leu
        195                  200                  205

Ala Asn Ser Thr Lys Leu Tyr Trp Leu Asn Leu Ser Phe Asn Ser Phe
    210                  215                  220

Ser Gly Pro Leu Pro Ala Ser Leu Thr His Ser Phe Ser Leu Thr Phe
```

```
     225                    230                    235                    240

 Leu Ser Leu Gln Asn Asn Asn Leu Ser Gly Ser Leu Pro Asn Ser Trp
                 245                    250                    255

 Gly Gly Asn Ser Lys Asn Gly Phe Phe Arg Leu Gln Asn Leu Ile Leu
                 260                    265                    270

 Asp His Asn Phe Phe Thr Gly Asp Val Pro Ala Ser Leu Gly Ser Leu
         275                    280                    285

 Arg Glu Leu Asn Glu Ile Ser Leu Ser His Asn Lys Phe Ser Gly Ala
     290                    295                    300

 Ile Pro Asn Glu Ile Gly Thr Leu Ser Arg Leu Lys Thr Leu Asp Ile
 305                    310                    315                    320

 Ser Asn Asn Ala Leu Asn Gly Asn Leu Pro Ala Thr Leu Ser Asn Leu
                 325                    330                    335

 Ser Ser Leu Thr Leu Leu Asn Ala Glu Asn Asn Leu Leu Asp Asn Gln
                 340                    345                    350

 Ile Pro Gln Ser Leu Gly Arg Leu Arg Asn Leu Ser Val Leu Ile Leu
                 355                    360                    365

 Ser Arg Asn Gln Phe Ser Gly His Ile Pro Ser Ser Ile Ala Asn Ile
     370                    375                    380

 Ser Ser Leu Arg Gln Leu Asp Leu Ser Leu Asn Asn Phe Ser Gly Glu
 385                    390                    395                    400

 Ile Pro Val Ser Phe Asp Ser Gln Arg Ser Leu Asn Leu Phe Asn Val
                 405                    410                    415

 Ser Tyr Asn Ser Leu Ser Gly Ser Val Pro Pro Leu Leu Ala Lys Lys
                 420                    425                    430

 Phe Asn Ser Ser Ser Phe Val Gly Asn Ile Gln Leu Cys Gly Tyr Ser
         435                    440                    445

 Pro Ser Thr Pro Cys Leu Ser Gln Ala Pro Ser Gln Gly Val Ile Ala
     450                    455                    460

 Pro Pro Pro Glu Val Ser Lys His His His His Arg Lys Leu Ser Thr
 465                    470                    475                    480

 Lys Asp Ile Ile Leu Ile Val Ala Gly Val Leu Leu Val Val Ile Ile
                 485                    490                    495

 Ile Leu Cys Cys Val Leu Leu Phe Cys Leu Ile Arg Lys Arg Ser Thr
                 500                    505                    510

 Ser Lys Ala Gly Asn Gly Gln Ala Thr Glu Gly Arg Ala Ala Thr Met
     515                    520                    525

 Arg Thr Glu Lys Gly Val Pro Pro Val Ala Gly Gly Asp Val Glu Ala
     530                    535                    540
```

Gly Gly Glu Ala Gly Gly Lys Leu Val His Phe Asp Gly Pro Met Ala
545   550   555   560

Phe Thr Ala Asp Asp Leu Leu Cys Ala Thr Ala Glu Ile Met Gly Lys
                565   570   575

Ser Thr Tyr Gly Thr Val Tyr Lys Ala Ile Leu Glu Asp Gly Ser Gln
            580   585   590

Val Ala Val Lys Arg Leu Arg Glu Lys Ile Thr Lys Gly His Arg Glu
        595   600   605

Phe Glu Ser Glu Val Ser Val Leu Gly Lys Ile Arg His Pro Asn Val
    610   615   620

Leu Ala Leu Arg Ala Tyr Tyr Leu Gly Pro Lys Gly Glu Lys Leu Leu
625   630   635   640

Val Phe Asp Tyr Met Ser Lys Gly Ser Leu Ala Ser Phe Leu His Gly
                645   650   655

Gly Gly Thr Glu Thr Phe Ile Asp Trp Pro Thr Arg Met Lys Ile Ala
                660   665   670

Gln Asp Leu Ala Arg Gly Leu Phe Cys Leu His Ser Gln Glu Asn Ile
            675   680   685

Ile His Gly Asn Leu Thr Ser Ser Asn Val Leu Leu Asp Glu Asn Thr
    690   695   700

Asn Ala Lys Ile Ala Asp Phe Gly Leu Ser Arg Leu Met Ser Thr Ala
705   710   715   720

Ala Asn Ser Asn Val Ile Ala Thr Ala Gly Ala Leu Gly Tyr Arg Ala
                725   730   735

Pro Glu Leu Ser Lys Leu Lys Lys Ala Asn Thr Lys Thr Asp Ile Tyr
            740   745   750

Ser Leu Gly Val Ile Leu Leu Glu Leu Leu Thr Arg Lys Ser Pro Gly
            755   760   765

Val Ser Met Asn Gly Leu Asp Leu Pro Gln Trp Val Ala Ser Val Val
    770   775   780

Lys Glu Glu Trp Thr Asn Glu Val Phe Asp Ala Asp Leu Met Arg Asp
785   790   795   800

Ala Ser Thr Val Gly Asp Glu Leu Leu Asn Thr Leu Lys Leu Ala Leu
                805   810   815

His Cys Val Asp Pro Ser Pro Ser Ala Arg Pro Glu Val His Gln Val
            820   825   830

Leu Gln Gln Leu Glu Glu Ile Arg Pro Glu Arg Ser Val Thr Ala Ser
        835   840   845

```
Pro Gly Asp Asp Ile Val
    850


<210>    1104
<211>    877
<212>    PRT
<213>    Glycine max

<223>    Seq ID: rhg1_toyosuzu_amplicon

<400>    1104

Met Asp Ala Cys Gly Met Ser Ser Ser Asn Ser Lys His Val Val Asp
1                   5                   10                  15

Gln Lys Arg Ser Thr Met Asn Met Met Ile Thr Thr Ile Leu Leu Arg
            20                  25                  30

Phe Trp Asp Arg Tyr Asp Met Asn Cys Asp Tyr Thr Thr Asn Ser Tyr
        35                  40                  45

Glu Pro Gly Thr Gln Leu Ala Pro Ser Ser Pro Arg Asp Thr Ser Val
    50                  55                  60

Lys Leu Gly Asp Ala Ser Ser Leu Val Val Leu Pro Ser Cys Val Arg
65                  70                  75                  80

Pro Val Leu Cys Glu Asp Glu Gly Trp Gly Val Val Val Thr Ala
            85                  90                  95

Ser Asn Leu Leu Ala Leu Glu Ala Phe Lys Gln Glu Leu Val Asp Pro
            100                 105                 110

Glu Gly Phe Leu Arg Ser Trp Asn Asp Ser Gly Tyr Gly Ala Cys Ser
        115                 120                 125

Gly Gly Trp Val Gly Ile Lys Cys Ala Gln Gly Gln Val Ile Val Ile
    130                 135                 140

Gln Leu Pro Trp Lys Gly Leu Arg Gly Arg Ile Thr Asp Lys Ile Gly
145                 150                 155                 160

Gln Leu Gln Gly Leu Arg Lys Leu Ser Leu His Asp Asn Gln Ile Gly
            165                 170                 175

Gly Ser Ile Pro Ser Thr Leu Gly Leu Leu Pro Asn Leu Arg Gly Val
        180                 185                 190

Gln Leu Phe Asn Asn Arg Leu Thr Gly Ser Ile Pro Leu Ser Leu Gly
        195                 200                 205

Phe Cys Pro Leu Leu Gln Ser Leu Asp Leu Ser Asn Asn Leu Leu Thr
    210                 215                 220

Gly Ala Ile Pro Tyr Ser Leu Ala Asn Ser Thr Lys Leu Tyr Trp Leu
225                 230                 235                 240
```

Asn Leu Ser Phe Asn Ser Phe Ser Gly Pro Leu Pro Ala Ser Leu Thr
            245   250   255

His Ser Phe Ser Leu Thr Phe Leu Ser Leu Gln Asn Asn Asn Leu Ser
            260   265   270

Gly Ser Leu Pro Asn Ser Trp Gly Gly Asn Ser Lys Asn Gly Phe Phe
            275   280   285

Arg Leu Gln Asn Leu Ile Leu Asp His Asn Phe Phe Thr Gly Asp Val
        290   295   300

Pro Ala Ser Leu Gly Ser Leu Arg Glu Leu Asn Glu Ile Ser Leu Ser
305   310   315   320

His Asn Lys Phe Ser Gly Ala Ile Pro Asn Glu Ile Gly Thr Leu Ser
                325   330   335

Arg Leu Lys Thr Leu Asp Ile Ser Asn Asn Ala Leu Asn Gly Asn Leu
            340   345   350

Pro Ala Thr Leu Ser Asn Leu Ser Ser Leu Thr Leu Leu Asn Ala Glu
            355   360   365

Asn Asn Leu Leu Asp Asn Gln Ile Pro Gln Ser Leu Gly Arg Leu Arg
        370   375   380

Asn Leu Ser Val Leu Ile Leu Ser Arg Asn Gln Phe Ser Gly His Ile
385   390   395   400

Pro Ser Ser Ile Ala Asn Ile Ser Ser Leu Arg Gln Leu Asp Leu Ser
                405   410   415

Leu Asn Asn Phe Ser Gly Glu Ile Pro Val Ser Phe Asp Ser Gln Arg
            420   425   430

Ser Leu Asn Leu Phe Asn Val Ser Tyr Asn Ser Leu Ser Gly Ser Val
            435   440   445

Pro Pro Leu Leu Ala Lys Lys Phe Asn Ser Ser Ser Phe Val Gly Asn
        450   455   460

Ile Gln Leu Cys Gly Tyr Ser Pro Ser Thr Pro Cys Leu Ser Gln Ala
465   470   475   480

Pro Ser Gln Gly Val Ile Ala Pro Pro Pro Glu Val Ser Lys His His
                485   490   495

His His Arg Lys Leu Ser Thr Lys Asp Ile Ile Leu Ile Val Ala Gly
            500   505   510

Val Leu Leu Val Val Leu Ile Ile Leu Cys Cys Val Leu Leu Phe Cys
        515   520   525

Leu Ile Arg Lys Arg Ser Thr Ser Lys Ala Gly Asn Gly Gln Ala Thr
        530   535   540

Glu Gly Arg Ala Ala Thr Met Arg Thr Glu Lys Gly Val Pro Pro Val

```
    545                  550                  555                    560

    Ala Gly Gly Asp Val Glu Ala Gly Gly Glu Ala Gly Gly Lys Leu Val
                  565                  570                  575

    His Phe Asp Gly Pro Met Ala Phe Thr Ala Asp Asp Leu Leu Cys Ala
                  580                  585                  590

    Thr Ala Glu Ile Met Gly Lys Ser Thr Tyr Gly Thr Val Tyr Lys Ala
              595                  600                  605

    Ile Leu Glu Asp Gly Ser Gln Val Ala Val Lys Arg Leu Arg Glu Lys
        610                  615                  620

    Ile Thr Lys Gly His Arg Glu Phe Glu Ser Glu Val Ser Val Leu Gly
    625                  630                  635                  640

    Lys Ile Arg His Pro Asn Val Leu Ala Leu Arg Ala Tyr Tyr Leu Gly
                  645                  650                  655

    Pro Lys Gly Glu Lys Leu Leu Val Phe Asp Tyr Met Ser Lys Gly Ser
                  660                  665                  670

    Leu Ala Ser Phe Leu His Gly Gly Gly Thr Glu Thr Phe Ile Asp Trp
            675                  680                  685

    Pro Thr Arg Met Lys Ile Ala Gln Asp Leu Ala Arg Gly Leu Phe Cys
        690                  695                  700

    Leu His Ser Gln Glu Asn Ile Ile His Gly Asn Leu Thr Ser Ser Asn
    705                  710                  715                  720

    Val Leu Leu Asp Glu Asn Thr Asn Ala Lys Ile Ala Asp Phe Gly Leu
                  725                  730                  735

    Ser Arg Leu Met Ser Thr Ala Ala Asn Ser Asn Val Ile Ala Thr Ala
              740                  745                  750

    Gly Ala Leu Gly Tyr Arg Ala Pro Glu Leu Ser Lys Leu Lys Lys Ala
            755                  760                  765

    Asn Thr Lys Thr Asp Ile Tyr Ser Leu Gly Val Ile Leu Leu Glu Leu
        770                  775                  780

    Leu Thr Arg Lys Ser Pro Gly Val Ser Met Asn Gly Leu Asp Leu Pro
    785                  790                  795                  800

    Gln Trp Val Ala Ser Val Val Lys Glu Glu Trp Thr Asn Glu Val Phe
                  805                  810                  815

    Asp Ala Asp Leu Met Arg Asp Ala Ser Thr Val Gly Asp Glu Leu Leu
                  820                  825                  830

    Asn Thr Leu Lys Leu Ala Leu His Cys Val Asp Pro Ser Pro Ser Ala
            835                  840                  845

    Arg Pro Glu Val His Gln Val Leu Gln Gln Leu Glu Glu Ile Arg Pro
        850                  855                  860
```

Glu Arg Ser Val Thr Ala Ser Pro Gly Asp Asp Ile Val
865   870   875

<210>   1105
<211>   854
<212>   PRT
<213>   Glycine max

<223>   Seq ID: rhg1_toyosuzu_amplicon

<400>   1105

Met Val Val Ala Val Glu Lys Thr Asn Leu Thr Ser Gln Ser Gln Cys
1   5   10   15

Phe Asn Arg Val Ser Asp Lys Lys Lys Glu Arg Cys Lys Thr His Met
            20   25   30

Asn Asn Val Asn Pro Cys Cys Phe Leu Phe Leu Leu Cys Val Trp Ser
        35   40   45

Leu Val Val Leu Pro Ser Cys Val Arg Pro Val Leu Cys Glu Asp Glu
    50   55   60

Gly Trp Asp Gly Val Val Val Thr Ala Ser Asn Leu Leu Ala Leu Glu
65   70   75   80

Ala Phe Lys Gln Glu Leu Val Asp Pro Glu Gly Phe Leu Arg Ser Trp
                85   90   95

Asn Asp Ser Gly Tyr Gly Ala Cys Ser Gly Gly Trp Val Gly Ile Lys
            100   105   110

Cys Ala Gln Gly Gln Val Ile Val Ile Gln Leu Pro Trp Lys Gly Leu
        115   120   125

Arg Gly Arg Ile Thr Asp Lys Ile Gly Gln Leu Gln Gly Leu Arg Lys
    130   135   140

Leu Ser Leu His Asp Asn Gln Ile Gly Gly Ser Ile Pro Ser Thr Leu
145   150   155   160

Gly Leu Leu Pro Asn Leu Arg Gly Val Gln Leu Phe Asn Asn Arg Leu
                165   170   175

Thr Gly Ser Ile Pro Leu Ser Leu Gly Phe Cys Pro Leu Leu Gln Ser
            180   185   190

Leu Asp Leu Ser Asn Asn Leu Leu Thr Gly Ala Ile Pro Tyr Ser Leu
        195   200   205

Ala Asn Ser Thr Lys Leu Tyr Trp Leu Asn Leu Ser Phe Asn Ser Phe
    210   215   220

Ser Gly Pro Leu Pro Ala Ser Leu Thr His Ser Phe Ser Leu Thr Phe

225   230   235   240

Leu Ser Leu Gln Asn Asn Asn Leu Ser Gly Ser Leu Pro Asn Ser Trp
                  245   250   255

Gly Gly Asn Ser Lys Asn Gly Phe Phe Arg Leu Gln Asn Leu Ile Leu
              260   265   270

Asp His Asn Phe Phe Thr Gly Asp Val Pro Ala Ser Leu Gly Ser Leu
          275   280   285

Arg Glu Leu Asn Glu Ile Ser Leu Ser His Asn Lys Phe Ser Gly Ala
      290   295   300

Ile Pro Asn Glu Ile Gly Thr Leu Ser Arg Leu Lys Thr Leu Asp Ile
305   310   315   320

Ser Asn Asn Ala Leu Asn Gly Asn Leu Pro Ala Thr Leu Ser Asn Leu
                  325   330   335

Ser Ser Leu Thr Leu Leu Asn Ala Glu Asn Asn Leu Leu Asp Asn Gln
              340   345   350

Ile Pro Gln Ser Leu Gly Arg Leu Arg Asn Leu Ser Val Leu Ile Leu
          355   360   365

Ser Arg Asn Gln Phe Ser Gly His Ile Pro Ser Ser Ile Ala Asn Ile
      370   375   380

Ser Ser Leu Arg Gln Leu Asp Leu Ser Leu Asn Asn Phe Ser Gly Glu
385   390   395   400

Ile Pro Val Ser Phe Asp Ser Gln Arg Ser Leu Asn Leu Phe Asn Val
                  405   410   415

Ser Tyr Asn Ser Leu Ser Gly Ser Val Pro Pro Leu Leu Ala Lys Lys
              420   425   430

Phe Asn Ser Ser Ser Phe Val Gly Asn Ile Gln Leu Cys Gly Tyr Ser
          435   440   445

Pro Ser Thr Pro Cys Leu Ser Gln Ala Pro Ser Gln Gly Val Ile Ala
      450   455   460

Pro Pro Pro Glu Val Ser Lys His His His His Arg Lys Leu Ser Thr
465   470   475   480

Lys Asp Ile Ile Leu Ile Val Ala Gly Val Leu Leu Val Val Leu Ile
                  485   490   495

Ile Leu Cys Cys Val Leu Leu Phe Cys Leu Ile Arg Lys Arg Ser Thr
          500   505   510

Ser Lys Ala Gly Asn Gly Gln Ala Thr Glu Gly Arg Ala Ala Thr Met
      515   520   525

Arg Thr Glu Lys Gly Val Pro Pro Val Ala Gly Gly Asp Val Glu Ala
      530   535   540

```
Gly Gly Glu Ala Gly Gly Lys Leu Val His Phe Asp Gly Pro Met Ala
545                 550                 555                 560

Phe Thr Ala Asp Asp Leu Leu Cys Ala Thr Ala Glu Ile Met Gly Lys
                565                 570                 575

Ser Thr Tyr Gly Thr Val Tyr Lys Ala Ile Leu Glu Asp Gly Ser Gln
            580                 585                 590

Val Ala Val Lys Arg Leu Arg Glu Lys Ile Thr Lys Gly His Arg Glu
        595                 600                 605

Phe Glu Ser Glu Val Ser Val Leu Gly Lys Ile Arg His Pro Asn Val
    610                 615                 620

Leu Ala Leu Arg Ala Tyr Tyr Leu Gly Pro Lys Gly Glu Lys Leu Leu
625                 630                 635                 640

Val Phe Asp Tyr Met Ser Lys Gly Ser Leu Ala Ser Phe Leu His Gly
                645                 650                 655

Gly Gly Thr Glu Thr Phe Ile Asp Trp Pro Thr Arg Met Lys Ile Ala
            660                 665                 670

Gln Asp Leu Ala Arg Gly Leu Phe Cys Leu His Ser Gln Glu Asn Ile
        675                 680                 685

Ile His Gly Asn Leu Thr Ser Ser Asn Val Leu Leu Asp Glu Asn Thr
    690                 695                 700

Asn Ala Lys Ile Ala Asp Phe Gly Leu Ser Arg Leu Met Ser Thr Ala
705                 710                 715                 720

Ala Asn Ser Asn Val Ile Ala Thr Ala Gly Ala Leu Gly Tyr Arg Ala
                725                 730                 735

Pro Glu Leu Ser Lys Leu Lys Lys Ala Asn Thr Lys Thr Asp Ile Tyr
            740                 745                 750

Ser Leu Gly Val Ile Leu Leu Gln Leu Leu Thr Arg Lys Ser Pro Gly
        755                 760                 765

Val Ser Met Asn Gly Leu Asp Leu Pro Gln Trp Val Ala Ser Val Val
    770                 775                 780

Lys Glu Glu Trp Thr Asn Glu Val Phe Asp Ala Asp Leu Met Arg Asp
785                 790                 795                 800

Ala Ser Thr Val Gly Asp Glu Leu Leu Asn Thr Leu Lys Leu Ala Leu
                805                 810                 815

His Cys Val Asp Pro Ser Pro Ser Ala Arg Pro Glu Val His Gln Val
            820                 825                 830

Leu Gln Gln Leu Glu Glu Ile Arg Pro Glu Arg Ser Val Thr Ala Ser
        835                 840                 845
```

Pro Gly Asp Asp Ile Val
    850

<210>   1106
<211>   877
<212>   PRT
<213>   Glycine max

<223>   Seq ID: rhg1_will_amplicon

<400>   1106

Met Asp Ala Cys Gly Met Ser Ser Ser Asn Ser Lys His Val Val Asp
1   5   10   15

Gln Lys Arg Ser Thr Met Asn Met Met Ile Thr Thr Ile Leu Leu Arg
            20   25   30

Phe Trp Asp Arg Tyr Asp Met Asn Cys Asp Tyr Thr Thr Asn Ser Tyr
        35   40   45

Glu Pro Gly Thr Gln Leu Ala Pro Ser Ser Pro Arg Asp Thr Ser Val
    50   55   60

Lys Leu Gly Asp Ala Ser Ser Leu Val Val Leu Pro Ser Cys Val Arg
65   70   75   80

Pro Val Leu Cys Glu Asp Glu Gly Trp Asp Gly Val Val Val Thr Ala
            85   90   95

Ser Asn Leu Leu Ala Leu Glu Ala Phe Lys Gln Glu Leu Val Asp Pro
            100   105   110

Glu Gly Phe Leu Arg Ser Trp Asn Asp Ser Gly Tyr Gly Ala Cys Ser
        115   120   125

Gly Gly Trp Val Gly Ile Lys Cys Ala Lys Gly Gln Val Ile Val Ile
    130   135   140

Gln Leu Pro Trp Lys Gly Leu Arg Gly Arg Ile Thr Asp Lys Ile Gly
145   150   155   160

Gln Leu Gln Gly Leu Arg Lys Leu Ser Leu His Asp Asn Gln Ile Gly
            165   170   175

Gly Ser Ile Pro Ser Thr Leu Gly Leu Leu Pro Asn Leu Arg Gly Val
            180   185   190

Gln Leu Phe Asn Asn Arg Leu Thr Gly Ser Ile Pro Leu Ser Leu Gly
        195   200   205

Phe Cys Pro Leu Leu Gln Ser Leu Asp Leu Ser Asn Asn Leu Leu Thr
    210   215   220

Gly Ala Ile Pro Tyr Ser Leu Ala Asn Ser Thr Lys Leu Tyr Trp Leu
225   230   235   240

```
Asn Leu Ser Phe Asn Ser Phe Ser Gly Pro Leu Pro Ala Ser Leu Thr
                245                 250                 255

His Ser Phe Ser Leu Thr Phe Leu Ser Leu Gln Asn Asn Asn Leu Ser
            260                 265                 270

Gly Ser Leu Pro Asn Ser Trp Gly Gly Asn Ser Lys Asn Gly Phe Phe
        275                 280                 285

Arg Leu Gln Asn Leu Ile Leu Asp His Asn Phe Phe Thr Gly Asp Val
    290                 295                 300

Pro Ala Ser Leu Gly Ser Leu Arg Glu Leu Asn Glu Ile Ser Leu Ser
305                 310                 315                 320

His Asn Lys Phe Ser Gly Ala Ile Pro Asn Glu Ile Gly Thr Leu Ser
            325                 330                 335

Arg Leu Lys Thr Leu Asp Ile Ser Asn Asn Ala Leu Asn Gly Asn Leu
            340                 345                 350

Pro Ala Thr Leu Ser Asn Leu Ser Ser Leu Thr Leu Leu Asn Ala Glu
        355                 360                 365

Asn Asn Leu Leu Asp Asn Gln Ile Pro Gln Ser Leu Gly Arg Leu Arg
    370                 375                 380

Asn Leu Ser Val Leu Ile Leu Ser Arg Asn Gln Phe Ser Gly His Ile
385                 390                 395                 400

Pro Ser Ser Ile Ala Asn Ile Ser Ser Leu Arg Gln Leu Asp Leu Ser
            405                 410                 415

Leu Asn Asn Phe Ser Gly Glu Ile Pro Val Ser Phe Asp Ser Gln Arg
        420                 425                 430

Ser Leu Asn Leu Phe Asn Val Ser Tyr Asn Ser Leu Ser Gly Ser Val
        435                 440                 445

Pro Pro Leu Leu Ala Lys Lys Phe Asn Ser Ser Ser Phe Val Gly Asn
    450                 455                 460

Ile Gln Leu Cys Gly Tyr Ser Pro Ser Thr Pro Cys Leu Ser Gln Ala
465                 470                 475                 480

Pro Ser Gln Gly Val Ile Ala Pro Pro Pro Glu Val Ser Lys His His
            485                 490                 495

His His Arg Lys Leu Ser Thr Lys Asp Ile Ile Leu Ile Val Ala Gly
        500                 505                 510

Val Leu Leu Val Val Leu Ile Ile Leu Cys Cys Val Leu Leu Phe Cys
        515                 520                 525

Leu Ile Arg Lys Arg Ser Thr Ser Lys Ala Gly Asn Gly Gln Ala Thr
    530                 535                 540

Glu Gly Arg Ala Ala Thr Met Arg Thr Glu Lys Gly Val Pro Pro Val
```

```
545                 550                 555                 560

Ala Gly Gly Asp Val Glu Ala Gly Gly Glu Ala Gly Gly Lys Leu Val
                565                 570                 575

His Phe Asp Gly Pro Met Ala Phe Thr Ala Asp Asp Leu Leu Cys Ala
                580                 585                 590

Thr Ala Glu Ile Met Gly Lys Ser Thr Tyr Gly Thr Val Tyr Lys Ala
            595                 600                 605

Ile Leu Glu Asp Gly Ser Gln Val Ala Val Lys Arg Leu Arg Glu Lys
        610                 615                 620

Ile Thr Lys Gly His Arg Glu Phe Glu Ser Glu Val Ser Val Leu Gly
    625                 630                 635                 640

Lys Ile Arg His Pro Asn Val Leu Ala Leu Arg Ala Tyr Tyr Leu Gly
                645                 650                 655

Pro Lys Gly Glu Lys Leu Leu Val Phe Asp Tyr Met Ser Lys Gly Ser
            660                 665                 670

Leu Ala Ser Phe Leu His Gly Gly Gly Thr Glu Thr Phe Ile Asp Trp
        675                 680                 685

Pro Thr Arg Met Lys Ile Ala Gln Asp Leu Ala Arg Gly Leu Phe Cys
    690                 695                 700

Leu His Ser Gln Glu Asn Ile Ile His Gly Asn Leu Thr Ser Ser Asn
705                 710                 715                 720

Val Leu Leu Asp Glu Asn Thr Asn Ala Lys Ile Ala Asp Phe Gly Leu
                725                 730                 735

Ser Arg Leu Met Ser Thr Ala Ala Asn Ser Asn Val Ile Ala Thr Ala
            740                 745                 750

Gly Ala Leu Gly Tyr Arg Ala Pro Glu Leu Ser Lys Leu Lys Lys Ala
        755                 760                 765

Asn Thr Lys Thr Asp Ile Tyr Ser Leu Gly Val Ile Leu Leu Glu Leu
    770                 775                 780

Leu Thr Arg Lys Ser Pro Gly Val Ser Met Asn Gly Leu Asp Leu Pro
785                 790                 795                 800

Gln Trp Val Ala Ser Val Val Lys Glu Glu Trp Thr Asn Glu Val Phe
                805                 810                 815

Asp Ala Asp Leu Met Arg Asp Ala Ser Thr Val Gly Asp Glu Leu Leu
            820                 825                 830

Asn Thr Leu Lys Leu Ala Leu His Cys Val Asp Pro Ser Pro Ser Ala
        835                 840                 845

Arg Pro Glu Val His Gln Val Leu Gln Gln Leu Glu Glu Ile Arg Pro
    850                 855                 860
```

```
Glu Arg Ser Val Thr Ala Ser Pro Gly Asp Asp Ile Val
865                 870                 875
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<211>      854
<212>      PRT
<213>      Glycine max

<223>      Seq ID: rhg1_will_amplicon

<400>      1107
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Met Val Val Ala Val Glu Lys Thr Asn Leu Thr Ser Gln Ser Gln Cys
1                   5                   10                  15

Phe Asn Arg Val Ser Asp Lys Lys Lys Glu Arg Cys Lys Thr His Met
            20                  25                  30

Asn Asn Val Asn Pro Cys Cys Phe Leu Phe Leu Leu Cys Val Trp Ser
        35                  40                  45

Leu Val Val Leu Pro Ser Cys Val Arg Pro Val Leu Cys Glu Asp Glu
    50                  55                  60

Gly Trp Asp Gly Val Val Thr Ala Ser Asn Leu Leu Ala Leu Glu
65                  70                  75                  80

Ala Phe Lys Gln Glu Leu Val Asp Pro Glu Gly Phe Leu Arg Ser Trp
                85                  90                  95

Asn Asp Ser Gly Tyr Gly Ala Cys Ser Gly Gly Trp Val Gly Ile Lys
            100                 105                 110

Cys Ala Lys Gly Gln Val Ile Val Ile Gln Leu Pro Trp Lys Gly Leu
        115                 120                 125

Arg Gly Arg Ile Thr Asp Lys Ile Gly Gln Leu Gln Gly Leu Arg Lys
    130                 135                 140

Leu Ser Leu His Asp Asn Gln Ile Gly Gly Ser Ile Pro Ser Thr Leu
145                 150                 155                 160

Gly Leu Leu Pro Asn Leu Arg Gly Val Gln Leu Phe Asn Asn Arg Leu
                165                 170                 175

Thr Gly Ser Ile Pro Leu Ser Leu Gly Phe Cys Pro Leu Leu Gln Ser
            180                 185                 190

Leu Asp Leu Ser Asn Asn Leu Leu Thr Gly Ala Ile Pro Tyr Ser Leu
        195                 200                 205

Ala Asn Ser Thr Lys Leu Tyr Trp Leu Asn Leu Ser Phe Asn Ser Phe
    210                 215                 220

Ser Gly Pro Leu Pro Ala Ser Leu Thr His Ser Phe Ser Leu Thr Phe
225                 230                 235                 240
```

Leu Ser Leu Gln Asn Asn Asn Leu Ser Gly Ser Leu Pro Asn Ser Trp
                245   250   255

Gly Gly Asn Ser Lys Asn Gly Phe Phe Arg Leu Gln Asn Leu Ile Leu
            260   265   270

Asp His Asn Phe Phe Thr Gly Asp Val Pro Ala Ser Leu Gly Ser Leu
        275   ·   280   285

Arg Glu Leu Asn Glu Ile Ser Ser Leu Ser His Asn Lys Phe Ser Gly Ala
    290   295   300

Ile Pro Asn Glu Ile Gly Thr Leu Ser Arg Leu Lys Thr Leu Asp Ile
305   310   315   320

Ser Asn Asn Ala Leu Asn Gly Asn Leu Pro Ala Thr Leu Ser Asn Leu
                325   330   335

Ser Ser Leu Thr Leu Leu Asn Ala Glu Asn Asn Leu Leu Asp Asn Gln
            340   345   350

Ile Pro Gln Ser Leu Gly Arg Leu Arg Asn Leu Ser Val Leu Ile Leu
        355   360   365

Ser Arg Asn Gln Phe Ser Gly His Ile Pro Ser Ser Ile Ala Asn Ile
    370   375   380

Ser Ser Leu Arg Gln Leu Asp Leu Ser Leu Asn Asn Phe Ser Gly Glu
385   390   395   400

Ile Pro Val Ser Phe Asp Ser Gln Arg Ser Leu Asn Leu Phe Asn Val
                405   410   415

Ser Tyr Asn Ser Leu Ser Gly Ser Val Pro Pro Leu Leu Ala Lys Lys
            420   425   430

Phe Asn Ser Ser Ser Phe Val Gly Asn Ile Gln Leu Cys Gly Tyr Ser
        435   440   445

Pro Ser Thr Pro Cys Leu Ser Gln Ala Pro Ser Gln Gly Val Ile Ala
    450   455   460

Pro Pro Pro Glu Val Ser Lys His His His His Arg Lys Leu Ser Thr
465   470   475   480

Lys Asp Ile Ile Leu Ile Val Ala Gly Val Leu Leu Val Val Leu Ile
                485   490   495

Ile Leu Cys Cys Val Leu Leu Phe Cys Leu Ile Arg Lys Arg Ser Thr
            500   505   510

Ser Lys Ala Gly Asn Gly Gln Ala Thr Glu Gly Arg Ala Ala Thr Met
        515   520   525

Arg Thr Glu Lys Gly Val Pro Pro Val Ala Gly Gly Asp Val Glu Ala
    530   535   540

```
Gly Gly Glu Ala Gly Gly Lys Leu Val His Phe Asp Gly Pro Met Ala
545                 550                 555                 560

Phe Thr Ala Asp Asp Leu Leu Cys Ala Thr Ala Glu Ile Met Gly Lys
                565                 570                 575

Ser Thr Tyr Gly Thr Val Tyr Lys Ala Ile Leu Glu Asp Gly Ser Gln
                580                 585                 590

Val Ala Val Lys Arg Leu Arg Glu Lys Ile Thr Lys Gly His Arg Glu
            595                 600                 605

Phe Glu Ser Glu Val Ser Val Leu Gly Lys Ile Arg His Pro Asn Val
    610                 615                 620

Leu Ala Leu Arg Ala Tyr Tyr Leu Gly Pro Lys Gly Glu Lys Leu Leu
625                 630                 635                 640

Val Phe Asp Tyr Met Ser Lys Gly Ser Leu Ala Ser Phe Leu His Gly
                645                 650                 655

Gly Gly Thr Glu Thr Phe Ile Asp Trp Pro Thr Arg Met Lys Ile Ala
                660                 665                 670

Gln Asp Leu Ala Arg Gly Leu Phe Cys Leu His Ser Gln Glu Asn Ile
        675                 680                 685

Ile His Gly Asn Leu Thr Ser Ser Asn Val Leu Leu Asp Glu Asn Thr
    690                 695                 700

Asn Ala Lys Ile Ala Asp Phe Gly Leu Ser Arg Leu Met Ser Thr Ala
705                 710                 715                 720

Ala Asn Ser Asn Val Ile Ala Thr Ala Gly Ala Leu Gly Tyr Arg Ala
                725                 730                 735

Pro Glu Leu Ser Lys Leu Lys Lys Ala Asn Thr Lys Thr Asp Ile Tyr
            740                 745                 750

Ser Leu Gly Val Ile Leu Leu Glu Leu Leu Thr Arg Lys Ser Pro Gly
        755                 760                 765

Val Ser Met Asn Gly Leu Asp Leu Pro Gln Trp Val Ala Ser Val Val
    770                 775                 780

Lys Glu Glu Trp Thr Asn Glu Val Phe Asp Ala Asp Leu Met Arg Asp
785                 790                 795                 800

Ala Ser Thr Val Gly Asp Glu Leu Leu Asn Thr Leu Lys Leu Ala Leu
                805                 810                 815

His Cys Val Asp Pro Ser Pro Ser Ala Arg Pro Glu Val His Gln Val
            820                 825                 830

Leu Gln Gln Leu Glu Glu Ile Arg Pro Glu Arg Ser Val Thr Ala Ser
        835                 840                 845

Pro Gly Asp Asp Ile Val
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850

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<210>      1108
<211>      877
<212>      PRT
<213>      Glycine max

<223>      Seq ID: rhg1_a2704_amplicon

<400>      1108


Met Asp Ala Cys Gly Met Ser Ser Ser Asn Ser Lys His Val Val Asp
1               5                   10                  15

Gln Lys Arg Ser Thr Met Asn Met Met Ile Thr Thr Ile Leu Leu Arg
            20                  25                  30

Phe Trp Asp Arg Tyr Asp Met Asn Cys Asp Tyr Thr Thr Asn Ser Tyr
        35                  40                  45

Glu Pro Gly Thr Gln Leu Ala Pro Ser Ser Pro Arg Asp Thr Ser Val
    50                  55                  60

Lys Leu Gly Asp Ala Ser Ser Leu Val Val Leu Pro Ser Cys Val Arg
65                  70                  75                  80

Pro Val Leu Cys Glu Asp Glu Gly Trp Asp Gly Val Val Val Thr Ala
            85                  90                  95

Ser Asn Leu Leu Ala Leu Glu Ala Phe Lys Gln Glu Leu Val Asp Pro
            100                 105                 110

Glu Gly Phe Leu Arg Ser Trp Asn Asp Ser Gly Tyr Gly Ala Cys Ser
        115                 120                 125

Gly Gly Trp Val Gly Ile Lys Cys Ala Lys Gly Gln Val Ile Val Ile
    130                 135                 140

Gln Leu Pro Trp Lys Gly Leu Arg Gly Arg Ile Thr Asp Lys Ile Gly
145                 150                 155                 160

Gln Leu Gln Gly Leu Arg Lys Leu Ser Leu His Asp Asn Gln Ile Gly
                165                 170                 175

Gly Ser Ile Pro Ser Thr Leu Gly Leu Leu Pro Asn Leu Arg Gly Val
            180                 185                 190

Gln Leu Phe Asn Asn Arg Leu Thr Gly Ser Ile Pro Leu Ser Leu Gly
        195                 200                 205

Phe Cys Pro Leu Leu Gln Ser Leu Asp Leu Ser Asn Asn Leu Leu Thr
    210                 215                 220

Gly Ala Ile Pro Tyr Ser Leu Ala Asn Ser Thr Lys Leu Tyr Trp Leu
225                 230                 235                 240

Asn Leu Ser Phe Asn Ser Phe Ser Gly Pro Leu Pro Ala Ser Leu Thr
```

```
                    245                  250                   255

His Ser Phe Ser Leu Thr Phe Leu Ser Leu Gln Asn Asn Asn Leu Ser
          260                  265                   270

Gly Ser Leu Pro Asn Ser Trp Gly Asn Ser Lys Asn Gly Phe Phe
      275                  280                  285

Arg Leu Gln Asn Leu Ile Leu Asp His Asn Phe Phe Thr Gly Asp Val
    290                  295                  300

Pro Ala Ser Leu Gly Ser Leu Arg Glu Leu Asn Glu Ile Ser Leu Ser
305                  310                  315                  320

His Asn Lys Phe Ser Gly Ala Ile Pro Asn Glu Ile Gly Thr Leu Ser
          325                  330                  335

Arg Leu Lys Thr Leu Asp Ile Ser Asn Ala Leu Asn Gly Asn Leu
          340                  345                  350

Pro Ala Thr Leu Ser Asn Leu Ser Ser Leu Thr Leu Leu Asn Ala Glu
      355                  360                  365

Asn Asn Leu Leu Asp Asn Gln Ile Pro Gln Ser Leu Gly Arg Leu Arg
      370                  375                  380

Asn Leu Ser Val Leu Ile Leu Ser Arg Asn Gln Phe Ser Gly His Ile
385                  390                  395                  400

Pro Ser Ser Ile Ala Asn Ile Ser Ser Leu Arg Gln Leu Asp Leu Ser
          405                  410                  415

Leu Asn Asn Phe Ser Gly Glu Ile Pro Val Ser Phe Asp Ser Gln Arg
          420                  425                  430

Ser Leu Asn Leu Phe Asn Val Ser Tyr Asn Ser Leu Ser Gly Ser Val
      435                  440                  445

Pro Pro Leu Leu Ala Lys Lys Phe Asn Ser Ser Ser Phe Val Gly Asn
    450                  455                  460

Ile Gln Leu Cys Gly Tyr Ser Pro Ser Thr Pro Cys Leu Ser Gln Ala
465                  470                  475                  480

Pro Ser Gln Gly Val Ile Ala Pro Pro Glu Val Ser Lys His His
          485                  490                  495

His His Arg Lys Leu Ser Thr Lys Asp Ile Ile Leu Ile Val Ala Gly
        500                  505                  510

Val Leu Leu Val Val Leu Ile Ile Leu Cys Cys Val Leu Leu Phe Cys
      515                  520                  525

Leu Ile Arg Lys Arg Ser Thr Ser Lys Ala Gly Asn Gly Gln Ala Thr
    530                  535                  540

Glu Gly Arg Ala Ala Thr Met Arg Thr Glu Lys Gly Val Pro Pro Val
545                  550                  555                  560
```

Ala Ala Gly Asp Val Glu Ala Gly Gly Glu Ala Gly Gly Lys Leu Val
                565   570   575

His Phe Asp Gly Pro Met Ala Phe Thr Ala Asp Asp Leu Leu Cys Ala
            580   585   590

Thr Ala Glu Ile Met Gly Lys Ser Thr Tyr Gly Thr Val Tyr Lys Ala
        595   600   605

Ile Leu Glu Asp Gly Ser Gln Val Ala Val Lys Arg Leu Arg Glu Lys
    610   615   620

Ile Thr Lys Gly His Arg Glu Phe Glu Ser Glu Val Ser Val Leu Gly
625   630   635   640

Lys Ile Arg His Pro Asn Val Leu Ala Leu Arg Ala Tyr Tyr Leu Gly
                645   650   655

Pro Lys Gly Lys Leu Leu Val Phe Asp Tyr Met Ser Asn Lys Gly Ser
            660   665   670

Leu Ala Ser Phe Leu His Gly Gly Gly Thr Glu Thr Phe Ile Asp Trp
        675   680   685

Pro Thr Arg Met Lys Ile Ala Gln Asp Leu Ala Arg Gly Leu Phe Cys
    690   695   700

Leu His Ser Gln Glu Asn Ile Ile His Gly Asn Leu Thr Ser Ser Asn
705   710   715   720

Val Leu Leu Asp Glu Asn Thr Asn Ala Lys Ile Ala Asp Phe Gly Leu
                725   730   735

Ser Arg Leu Met Ser Thr Ala Ala Asn Ser Asn Val Ile Ala Thr Ala
            740   745   750

Gly Ala Leu Gly Tyr Arg Ala Pro Glu Leu Ser Lys Leu Lys Lys Ala
        755   760   765

Asn Thr Lys Thr Asp Ile Tyr Ser Leu Gly Val Ile Leu Leu Glu Leu
    770   775   780

Leu Thr Arg Lys Ser Pro Gly Val Pro Met Asn Gly Leu Asp Leu Pro
785   790   795   800

Gln Trp Val Ala Ser Val Val Lys Glu Glu Trp Thr Asn Glu Val Phe
                805   810   815

Asp Ala Asp Leu Met Arg Asp Ala Ser Thr Val Gly Asp Glu Leu Leu
            820   825   830

Asn Thr Leu Lys Leu Ala Leu His Cys Val Asp Pro Ser Pro Ser Ala
        835   840   845

Arg Pro Glu Val His Gln Val Leu Gln Gln Leu Glu Glu Ile Arg Pro
    850   855   860

```
Glu Arg Ser Val Thr Ala Ser Pro Gly Asp Asp Ile Val
865                 870                 875


<210>      1109
<211>      854
<212>      PRT
<213>      Glycine max

<223>      Seq ID: rhg1_a2704_amplicon

<400>      1109

Met Val Val Ala Val Glu Lys Thr Asn Leu Thr Ser Gln Ser Gln Cys
1               5                   10                  15

Phe Asn Arg Val Ser Asp Lys Lys Lys Glu Arg Cys Lys Thr His Met
            20                  25                  30

Asn Asn Val Asn Pro Cys Cys Phe Leu Phe Leu Leu Cys Val Trp Ser
        35                  40                  45

Leu Val Val Leu Pro Ser Cys Val Arg Pro Val Leu Cys Glu Asp Glu
    50                  55                  60

Gly Trp Asp Gly Val Val Val Thr Ala Ser Asn Leu Leu Ala Leu Glu
65                  70                  75                  80

Ala Phe Lys Gln Glu Leu Val Asp Pro Glu Gly Phe Leu Arg Ser Trp
            85                  90                  95

Asn Asp Ser Gly Tyr Gly Ala Cys Ser Gly Gly Trp Val Gly Ile Lys
            100                 105                 110

Cys Ala Lys Gly Gln Val Ile Val Ile Gln Leu Pro Trp Lys Gly Leu
        115                 120                 125

Arg Gly Arg Ile Thr Asp Lys Ile Gly Gln Leu Gln Gly Leu Arg Lys
    130                 135                 140

Leu Ser Leu His Asp Asn Gln Ile Gly Gly Ser Ile Pro Ser Thr Leu
145                 150                 155                 160

Gly Leu Leu Pro Asn Leu Arg Gly Val Gln Leu Phe Asn Asn Arg Leu
            165                 170                 175

Thr Gly Ser Ile Pro Leu Ser Leu Gly Phe Cys Pro Leu Leu Gln Ser
            180                 185                 190

Leu Asp Leu Ser Asn Asn Leu Leu Thr Gly Ala Ile Pro Tyr Ser Leu
        195                 200                 205

Ala Asn Ser Thr Lys Leu Tyr Trp Leu Asn Leu Ser Phe Asn Ser Phe
    210                 215                 220

Ser Gly Pro Leu Pro Ala Ser Leu Thr His Ser Phe Ser Leu Thr Phe
225                 230                 235                 240
```

Leu Ser Leu Gln Asn Asn Asn Leu Ser Gly Ser Leu Pro Asn Ser Trp
                245   250   255

Gly Gly Asn Ser Lys Asn Gly Phe Phe Arg Leu Gln Asn Leu Ile Leu
            260   265   270

Asp His Asn Phe Phe Thr Gly Asp Val Pro Ala Ser Leu Gly Ser Leu
        275   280   285

Arg Glu Leu Asn Glu Ile Ser Leu Ser His Asn Lys Phe Ser Gly Ala
    290   295   300

Ile Pro Asn Glu Ile Gly Thr Leu Ser Arg Leu Lys Thr Leu Asp Ile
305   310   315   320

Ser Asn Asn Ala Leu Asn Gly Asn Leu Pro Ala Thr Leu Ser Asn Leu
            325   330   335

Ser Ser Leu Thr Leu Leu Asn Ala Glu Asn Asn Leu Leu Asp Asn Gln
        340   345   350

Ile Pro Gln Ser Leu Gly Arg Leu Arg Asn Leu Ser Val Leu Ile Leu
        355   360   365

Ser Arg Asn Gln Phe Ser Gly His Ile Pro Ser Ser Ile Ala Asn Ile
    370   375   380

Ser Ser Leu Arg Gln Leu Asp Leu Ser Leu Asn Asn Phe Ser Gly Glu
385   390   395   400

Ile Pro Val Ser Phe Asp Ser Gln Arg Ser Leu Asn Leu Phe Asn Val
            405   410   415

Ser Tyr Asn Ser Leu Ser Gly Ser Val Pro Pro Leu Leu Ala Lys Lys
        420   425   430

Phe Asn Ser Ser Ser Phe Val Gly Asn Ile Gln Leu Cys Gly Tyr Ser
        435   440   445

Pro Ser Thr Pro Cys Leu Ser Gln Ala Pro Ser Gln Gly Val Ile Ala
    450   455   460

Pro Pro Pro Glu Val Ser Lys His His His His Arg Lys Leu Ser Thr
465   470   475   480

Lys Asp Ile Ile Leu Ile Val Ala Gly Val Leu Leu Val Val Leu Ile
            485   490   495

Ile Leu Cys Cys Val Leu Leu Phe Cys Leu Ile Arg Lys Arg Ser Thr
        500   505   510

Ser Lys Ala Gly Asn Gly Gln Ala Thr Glu Gly Arg Ala Ala Thr Met
    515   520   525

Arg Thr Glu Lys Gly Val Pro Pro Val Ala Ala Gly Asp Val Glu Ala
530   535   540

Gly Gly Glu Ala Gly Gly Lys Leu Val His Phe Asp Gly Pro Met Ala

```
   545                    550                    555                    560

   Phe Thr Ala Asp Asp Leu Leu Cys Ala Thr Ala Glu Ile Met Gly Lys
                  565                    570                    575

   Ser Thr Tyr Gly Thr Val Tyr Lys Ala Ile Leu Glu Asp Gly Ser Gln
                  580                    585                    590

   Val Ala Val Lys Arg Leu Arg Glu Lys Ile Thr Lys Gly His Arg Glu
                  595                    600                    605

   Phe Glu Ser Glu Val Ser Val Leu Gly Lys Ile Arg His Pro Asn Val
       610                    615                    620

   Leu Ala Leu Arg Ala Tyr Tyr Leu Gly Pro Lys Gly Glu Lys Leu Leu
   625                    630                    635                    640

   Val Phe Asp Tyr Met Ser Lys Gly Ser Leu Ala Ser Phe Leu His Gly
                  645                    650                    655

   Gly Gly Thr Glu Thr Phe Ile Asp Trp Pro Thr Arg Met Lys Ile Ala
                  660                    665                    670

   Gln Asp Leu Ala Arg Gly Leu Phe Cys Leu His Ser Gln Glu Asn Ile
       675                    680                    685

   Ile His Gly Asn Leu Thr Ser Ser Asn Val Leu Leu Asp Glu Asn Thr
       690                    695                    700

   Asn Ala Lys Ile Ala Asp Phe Gly Leu Ser Arg Leu Met Ser Thr Ala
   705                    710                    715                    720

   Ala Asn Ser Asn Val Ile Ala Thr Ala Gly Ala Leu Gly Tyr Arg Ala
                  725                    730                    735

   Pro Glu Leu Ser Lys Leu Lys Lys Ala Asn Thr Lys Thr Asp Ile Tyr
                  740                    745                    750

   Ser Leu Gly Val Ile Leu Leu Glu Leu Leu Thr Arg Lys Ser Pro Gly
                  755                    760                    765

   Val Pro Met Asn Gly Leu Asp Leu Pro Gln Trp Val Ala Ser Val Val
       770                    775                    780

   Lys Glu Glu Trp Thr Asn Glu Val Phe Asp Ala Asp Leu Met Arg Asp
   785                    790                    795                    800

   Ala Ser Thr Val Gly Asp Glu Leu Leu Asn Thr Leu Lys Leu Ala Leu
                  805                    810                    815

   His Cys Val Asp Pro Ser Pro Ser Ala Arg Pro Glu Val His Gln Val
                  820                    825                    830

   Leu Gln Gln Leu Glu Glu Ile Arg Pro Glu Arg Ser Val Thr Ala Ser
       835                    840                    845

   Pro Gly Asp Asp Ile Val
       850
```

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<210>      1110
<211>      877
<212>      PRT
<213>      Glycine max

<223>      Seq ID: rhg1_noir_amplicon

<400>      1110
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Met Asp Ala Tyr Gly Met Ser Ser Ser Asn Ser Lys His Val Val Asp
1   5   10   15

Gln Lys Arg Ser Thr Met Asn Met Met Ile Thr Thr Ile Leu Leu Arg
            20   25   30

Phe Trp Asp Arg Tyr Asp Met Asn Cys Asp Tyr Thr Thr Asn Ser Tyr
         35   40   45

Glu Pro Gly Thr Gln Leu Ala Pro Ser Ser Pro Arg Asp Thr Ser Val
    50   55   60

Lys Leu Gly Asp Ala Ser Ser Leu Val Val Leu Pro Ser Cys Val Arg
65   70   75   80

Pro Val Leu Cys Glu Asp Glu Gly Trp Asp Gly Val Val Val Thr Ala
                85   90   95

Ser Asn Leu Leu Ala Leu Glu Ala Phe Lys Gln Glu Leu Val Asp Pro
            100   105   110

Glu Gly Phe Leu Arg Ser Trp Asn Asp Ser Gly Tyr Gly Ala Cys Ser
         115   120   125

Gly Gly Trp Val Gly Ile Lys Cys Ala Gln Gly Gln Val Ile Val Ile
    130   135   140

Gln Leu Pro Trp Lys Gly Leu Arg Gly Arg Ile Thr Asp Lys Ile Gly
145   150   155   160

Gln Leu Gln Gly Leu Arg Lys Leu Ser Leu His Asp Asn Gln Ile Gly
                165   170   175

Gly Ser Ile Pro Ser Thr Leu Gly Leu Leu Pro Asn Leu Arg Gly Val
            180   185   190

Gln Leu Phe Asn Asn Arg Leu Thr Gly Ser Ile Pro Leu Ser Leu Gly
         195   200   205

Phe Cys Pro Leu Leu Gln Ser Leu Asp Leu Ser Asn Asn Leu Leu Thr
    210   215   220

Gly Ala Ile Pro Tyr Ser Leu Ala Asn Ser Thr Lys Leu Tyr Trp Leu
225   230   235   240

Asn Leu Ser Phe Asn Ser Phe Ser Gly Pro Leu Pro Ala Ser Leu Thr
            245   250   255

```
His Ser Phe Ser Leu Thr Phe Leu Ser Leu Gln Asn Asn Asn Leu Ser
              260                 265                 270

Gly Ser Leu Pro Asn Ser Trp Gly Gly Asn Ser Lys Asn Gly Phe Phe
              275                 280                 285

Arg Leu Gln Asn Leu Ile Leu Asp Asn Asn Phe Phe Thr Gly Asp Val
    290                 295                 300

Pro Ala Ser Leu Gly Ser Leu Arg Glu Leu Asn Glu Ile Ser Leu Ser
305                 310                 315                 320

His Asn Lys Phe Ser Gly Ala Ile Pro Asn Glu Ile Gly Thr Leu Ser
              325                 330                 335

Arg Leu Lys Thr Leu Asp Ile Ser Asn Asn Ala Leu Asn Gly Asn Leu
              340                 345                 350

Pro Ala Thr Leu Ser Asn Leu Ser Ser Leu Thr Leu Leu Asn Ala Glu
              355                 360                 365

Asn Asn Leu Leu Asp Asn Gln Ile Pro Gln Ser Leu Gly Arg Leu Arg
    370                 375                 380

Asn Leu Ser Val Leu Ile Leu Ser Arg Asn Gln Phe Ser Gly His Ile
385                 390                 395                 400

Pro Ser Ser Ile Ala Asn Ile Ser Ser Leu Arg Gln Leu Asp Leu Ser
              405                 410                 415

Leu Asn Asn Phe Ser Gly Glu Ile Pro Val Ser Phe Asp Ser Gln Arg
              420                 425                 430

Ser Leu Asn Leu Phe Asn Val Ser Tyr Asn Ser Leu Ser Gly Ser Val
              435                 440                 445

Pro Pro Leu Leu Ala Lys Lys Phe Asn Ser Ser Ser Phe Val Gly Asn
    450                 455                 460

Ile Gln Leu Cys Gly Tyr Ser Pro Ser Thr Pro Cys Leu Ser Gln Ala
465                 470                 475                 480

Pro Ser Gln Gly Val Ile Ala Pro Pro Glu Val Ser Lys His His
              485                 490                 495

His His Arg Lys Leu Ser Thr Lys Asp Ile Ile Leu Ile Val Ala Gly
              500                 505                 510

Val Leu Leu Val Val Leu Ile Ile Leu Cys Cys Val Leu Leu Phe Cys
              515                 520                 525

Leu Ile Arg Lys Arg Ser Thr Ser Lys Ala Gly Asn Gly Gln Ala Thr
    530                 535                 540

Glu Gly Arg Ala Ala Thr Met Arg Thr Glu Lys Gly Val Pro Pro Val
545                 550                 555                 560
```

1191

Ala Ala Gly Asp Val Glu Ala Gly Gly Glu Ala Gly Gly Lys Leu Val
                565   570   575

His Phe Asp Gly Pro Met Ala Phe Thr Ala Asp Asp Leu Leu Cys Ala
                580   585   590

Thr Ala Glu Ile Met Gly Lys Ser Thr Tyr Gly Thr Val Tyr Lys Ala
                595   600   605

Ile Leu Glu Asp Gly Ser Gln Val Ala Val Lys Arg Leu Arg Glu Lys
        610   615   620

Ile Thr Lys Gly His Arg Glu Phe Glu Ser Glu Val Ser Val Leu Gly
625   630   635   640

Lys Ile Arg His Pro Asn Val Leu Ala Leu Arg Ala Tyr Tyr Leu Gly
                645   650   655

Pro Lys Gly Glu Lys Leu Leu Val Phe Asp Tyr Met Ser Lys Gly Ser
                660   665   670

Leu Ala Ser Phe Leu His Gly Gly Gly Thr Glu Thr Phe Ile Asp Trp
        675   680   685

Pro Thr Arg Met Lys Ile Ala Gln Asp Leu Ala Arg Gly Leu Phe Cys
        690   695   700

Leu His Ser Gln Glu Asn Ile Ile His Gly Asn Leu Thr Ser Ser Asn
705   710   715   720

Val Leu Leu Asp Glu Asn Thr Asn Ala Lys Ile Ala Asp Phe Gly Leu
                725   730   735

Ser Arg Leu Met Ser Thr Ala Ala Asn Ser Asn Val Ile Ala Thr Ala
        740   745   750

Gly Ala Leu Gly Tyr Arg Ala Pro Glu Leu Ser Lys Leu Lys Lys Ala
        755   760   765

Asn Thr Lys Thr Asp Ile Tyr Ser Leu Gly Val Ile Leu Leu Glu Leu
        770   775   780

Leu Thr Arg Lys Ser Pro Gly Val Pro Met Asn Gly Leu Asp Leu Pro
785   790   795   800

Gln Trp Val Ala Ser Val Val Lys Glu Glu Trp Thr Asn Glu Val Phe
                805   810   815

Asp Ala Asp Leu Met Arg Asp Ala Ser Thr Val Gly Asp Glu Leu Leu
        820   825   830

Asn Thr Leu Lys Leu Ala Leu His Cys Val Asp Pro Ser Pro Ser Ala
        835   840   845

Arg Pro Glu Val His Gln Val Leu Gln Gln Leu Glu Glu Ile Arg Pro
850   855   860

Glu Arg Ser Val Thr Ala Ser Pro Gly Asp Asp Ile Val

865   870   875


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<210>     1111
<211>     854
<212>     PRT
<213>     Glycine max

<223>     Seq ID: rhg1_noir_amplicon

<400>     1111
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Met Val Val Ala Val Glu Lys Thr Asn Leu Thr Ser Gln Ser Gln Cys
1   5   10   15

Phe Asn Arg Val Ser Asp Lys Lys Lys Glu Arg Cys Lys Thr His Met
            20   25   30

Asn Asn Val Asn Pro Cys Cys Phe Leu Phe Leu Leu Cys Val Trp Ser
        35   40   45

Leu Val Val Leu Pro Ser Cys Val Arg Pro Val Leu Cys Glu Asp Glu
    50   55   60

Gly Trp Asp Gly Val Val Thr Ala Ser Asn Leu Leu Ala Leu Glu
65   70   75   80

Ala Phe Lys Gln Glu Leu Val Asp Pro Glu Gly Phe Leu Arg Ser Trp
            85   90   95

Asn Asp Ser Gly Tyr Gly Ala Cys Ser Gly Gly Trp Val Gly Ile Lys
            100   105   110

Cys Ala Gln Gly Gln Val Ile Val Ile Gln Leu Pro Trp Lys Gly Leu
        115   120   125

Arg Gly Arg Ile Thr Asp Lys Ile Gly Gln Leu Gln Gly Leu Arg Lys
    130   135   140

Leu Ser Leu His Asp Asn Gln Ile Gly Gly Ser Ile Pro Ser Thr Leu
145   150   155   160

Gly Leu Leu Pro Asn Leu Arg Gly Val Gln Leu Phe Asn Asn Arg Leu
            165   170   175

Thr Gly Ser Ile Pro Leu Ser Leu Gly Phe Cys Pro Leu Leu Gln Ser
        180   185   190

Leu Asp Leu Ser Asn Asn Leu Leu Thr Gly Ala Ile Pro Tyr Ser Leu
    195   200   205

Ala Asn Ser Thr Lys Leu Tyr Trp Leu Asn Leu Ser Phe Asn Ser Phe
    210   215   220

Ser Gly Pro Leu Pro Ala Ser Leu Thr His Ser Phe Ser Leu Thr Phe
225   230   235   240

Leu Ser Leu Gln Asn Asn Asn Leu Ser Gly Ser Leu Pro Asn Ser Trp

```
                    245                    250                    255

  Gly Gly Asn Ser Lys Asn Gly Phe Phe Arg Leu Gln Asn Leu Ile Leu
                260                    265                    270

  Asp Asn Asn Phe Phe Thr Gly Asp Val Pro Ala Ser Leu Gly Ser Leu
            275                    280                    285

  Arg Glu Leu Asn Glu Ile Ser Leu Ser His Asn Lys Phe Ser Gly Ala
      290                    295                    300

  Ile Pro Asn Glu Ile Gly Thr Leu Ser Arg Leu Lys Thr Leu Asp Ile
  305                    310                    315                    320

  Ser Asn Asn Ala Leu Asn Gly Asn Leu Pro Ala Thr Leu Ser Asn Leu
                325                    330                    335

  Ser Ser Leu Thr Leu Leu Asn Ala Glu Asn Asn Leu Leu Asp Asn Gln
            340                    345                    350

  Ile Pro Gln Ser Leu Gly Arg Leu Arg Asn Leu Ser Val Leu Ile Leu
      355                    360                    365

  Ser Arg Asn Gln Phe Ser Gly His Ile Pro Ser Ser Ile Ala Asn Ile
      370                    375                    380

  Ser Ser Leu Arg Gln Leu Asp Leu Ser Leu Asn Asn Phe Ser Gly Glu
  385                    390                    395                    400

  Ile Pro Val Ser Phe Asp Ser Gln Arg Ser Leu Asn Leu Phe Asn Val
                405                    410                    415

  Ser Tyr Asn Ser Leu Ser Gly Ser Val Pro Pro Leu Leu Ala Lys Lys
                420                    425                    430

  Phe Asn Ser Ser Ser Phe Val Gly Asn Ile Gln Leu Cys Gly Tyr Ser
            435                    440                    445

  Pro Ser Thr Pro Cys Leu Ser Gln Ala Pro Ser Gln Gly Val Ile Ala
      450                    455                    460

  Pro Pro Pro Glu Val Ser Lys His His His His Arg Lys Leu Ser Thr
  465                    470                    475                    480

  Lys Asp Ile Ile Leu Ile Val Ala Gly Val Leu Leu Val Val Leu Ile
                485                    490                    495

  Ile Leu Cys Cys Val Leu Leu Phe Cys Leu Ile Arg Lys Arg Ser Thr
            500                    505                    510

  Ser Lys Ala Gly Asn Gly Gln Ala Thr Glu Gly Arg Ala Ala Thr Met
      515                    520                    525

  Arg Thr Glu Lys Gly Val Pro Pro Val Ala Ala Gly Asp Val Glu Ala
      530                    535                    540

  Gly Gly Glu Ala Gly Gly Lys Leu Val His Phe Asp Gly Pro Met Ala
  545                    550                    555                    560
```

Phe Thr Ala Asp Asp Leu Leu Cys Ala Thr Ala Glu Ile Met Gly Lys
                565   570   575

Ser Thr Tyr Gly Thr Val Tyr Lys Ala Ile Leu Glu Asp Gly Ser Gln
            580   585   590

Val Ala Val Lys Arg Leu Arg Glu Lys Ile Thr Lys Gly His Arg Glu
        595   600   605

Phe Glu Ser Glu Val Ser Val Leu Gly Lys Ile Arg His Pro Asn Val
    610   615   620

Leu Ala Leu Arg Ala Tyr Tyr Leu Gly Pro Lys Gly Glu Lys Leu Leu
625   630   635   640

Val Phe Asp Tyr Met Ser Lys Gly Ser Leu Ala Ser Phe Leu His Gly
                645   650   655

Gly Gly Thr Glu Thr Phe Ile Asp Trp Pro Thr Arg Met Lys Ile Ala
            660   665   670

Gln Asp Leu Ala Arg Gly Leu Phe Cys Leu His Ser Gln Glu Asn Ile
        675   680   685

Ile His Gly Asn Leu Thr Ser Ser Asn Val Leu Leu Asp Glu Asn Thr
    690   695   700

Asn Ala Lys Ile Ala Asp Phe Gly Leu Ser Arg Leu Met Ser Thr Ala
705   710   715   720

Ala Asn Ser Asn Val Ile Ala Thr Ala Gly Ala Leu Gly Tyr Arg Ala
                725   730   735

Pro Glu Leu Ser Lys Leu Lys Lys Ala Asn Thr Lys Thr Asp Ile Tyr
            740   745   750

Ser Leu Gly Val Ile Leu Leu Glu Leu Leu Thr Arg Lys Ser Pro Gly
            755   760   765

Val Pro Met Asn Gly Leu Asp Leu Pro Gln Trp Val Ala Ser Val Val
    770   775   780

Lys Glu Glu Trp Thr Asn Glu Val Phe Asp Ala Asp Leu Met Arg Asp
785   790   795   800

Ala Ser Thr Val Gly Asp Glu Leu Leu Asn Thr Leu Lys Leu Ala Leu
                805   810   815

His Cys Val Asp Pro Ser Pro Ser Ala Arg Pro Glu Val His Gln Val
            820   825   830

Leu Gln Gln Leu Glu Glu Ile Arg Pro Glu Arg Ser Val Thr Ala Ser
        835   840   845

Pro Gly Asp Asp Ile Val
    850

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<210>      1112
<211>      877
<212>      PRT
<213>      Glycine max

<223>      Seq ID: rhg1_lee_amplicon

<400>      1112
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Met Asp Ala Tyr Gly Met Ser Ser Ser Asn Ser Lys His Val Val Asp
1               5                   10                  15

Gln Lys Arg Ser Thr Met Asn Met Met Ile Thr Thr Ile Leu Leu Arg
            20                  25                  30

Phe Trp Asp Arg Tyr Asp Met Asn Cys Asp Tyr Thr Thr Asn Ser Tyr
        35                  40                  45

Glu Pro Gly Thr Gln Leu Ala Pro Ser Ser Pro Arg Asp Thr Ser Val
    50                  55                  60

Lys Leu Gly Asp Ala Ser Ser Leu Val Val Leu Pro Ser Cys Val Arg
65                  70                  75                  80

Pro Val Leu Cys Glu Asp Glu Gly Trp Asp Gly Val Val Val Thr Ala
                85                  90                  95

Ser Asn Leu Leu Ala Leu Glu Ala Phe Lys Gln Glu Leu Val Asp Pro
            100                 105                 110

Glu Gly Phe Leu Arg Ser Trp Asn Asp Ser Gly Tyr Gly Ala Cys Ser
        115                 120                 125

Gly Gly Trp Val Gly Ile Lys Cys Ala Gln Gly Gln Val Ile Val Ile
    130                 135                 140

Gln Leu Pro Trp Lys Gly Leu Arg Gly Arg Ile Thr Asp Lys Ile Gly
145                 150                 155                 160

Gln Leu Gln Gly Leu Arg Lys Leu Ser Leu His Asp Asn Gln Ile Gly
            165                 170                 175

Gly Ser Ile Pro Ser Thr Leu Gly Leu Leu Pro Asn Leu Arg Gly Val
        180                 185                 190

Gln Leu Phe Asn Asn Arg Leu Thr Gly Ser Ile Pro Leu Ser Leu Gly
        195                 200                 205

Phe Cys Pro Leu Leu Gln Ser Leu Asp Leu Ser Asn Asn Leu Leu Thr
    210                 215                 220

Gly Ala Ile Pro Tyr Ser Leu Ala Asn Ser Thr Lys Leu Tyr Trp Leu
225                 230                 235                 240

Asn Leu Ser Phe Asn Ser Phe Ser Gly Pro Leu Pro Ala Ser Leu Thr
            245                 250                 255
```

His Ser Phe Ser Leu Thr Phe Leu Ser Leu Gln Asn Asn Asn Leu Ser
            260   265   270

Gly Ser Leu Pro Asn Ser Trp Gly Gly Asn Ser Lys Asn Gly Phe Phe
            275   280   285

Arg Leu Gln Asn Leu Ile Leu Asp Asn Asn Phe Phe Thr Gly Asp Val
    290   295   300

Pro Ala Ser Leu Gly Ser Leu Arg Glu Leu Asn Glu Ile Ser Leu Ser
305   310   315   320

His Asn Lys Phe Ser Gly Ala Ile Pro Asn Glu Ile Gly Thr Leu Ser
            325   330   335

Arg Leu Lys Thr Leu Asp Ile Ser Asn Asn Ala Leu Asn Gly Asn Leu
            340   345   350

Pro Ala Thr Leu Ser Asn Leu Ser Ser Leu Thr Leu Leu Asn Ala Glu
            355   360   365

Asn Asn Leu Leu Asp Asn Gln Ile Pro Gln Ser Leu Gly Arg Leu Arg
    370   375   380

Asn Leu Ser Val Leu Ile Leu Ser Arg Asn Gln Phe Ser Gly His Ile
385   390   395   400

Pro Ser Ser Ile Ala Asn Ile Ser Ser Leu Arg Gln Leu Asp Leu Ser
            405   410   415

Leu Asn Asn Phe Ser Gly Glu Ile Pro Val Ser Phe Asp Ser Gln Arg
            420   425   430

Ser Leu Asn Leu Phe Asn Val Ser Tyr Asn Ser Leu Ser Gly Ser Val
            435   440   445

Pro Pro Leu Leu Ala Lys Lys Phe Asn Ser Ser Ser Phe Val Gly Asn
    450   455   460

Ile Gln Leu Cys Gly Tyr Ser Pro Ser Thr Pro Cys Leu Ser Gln Ala
465   470   475   480

Pro Ser Gln Gly Val Ile Ala Pro Pro Glu Val Ser Lys His His
            485   490   495

His His Arg Lys Leu Ser Thr Lys Asp Ile Ile Leu Ile Val Ala Gly
            500   505   510

Val Leu Leu Val Val Leu Ile Ile Leu Cys Cys Val Leu Leu Phe Cys
            515   520   525

Leu Ile Arg Lys Arg Ser Thr Ser Lys Ala Gly Asn Gly Gln Ala Thr
    530   535   540

Glu Gly Arg Ala Ala Thr Met Arg Thr Glu Lys Gly Val Pro Pro Val
545   550   555   560

Ala Ala Gly Asp Val Glu Ala Gly Gly Glu Ala Gly Gly Lys Leu Val

```
                    565                 570                 575

    His Phe Asp Gly Pro Met Ala Phe Thr Ala Asp Asp Leu Leu Cys Ala
                580                 585                 590

    Thr Ala Glu Ile Met Gly Lys Ser Thr Tyr Gly Thr Val Tyr Lys Ala
            595                 600                 605

    Ile Leu Glu Asp Gly Ser Gln Val Ala Val Lys Arg Leu Arg Glu Lys
        610                 615                 620

    Ile Thr Lys Gly His Arg Glu Phe Glu Ser Glu Val Ser Val Leu Gly
    625                 630                 635                 640

    Lys Ile Arg His Pro Asn Val Leu Ala Leu Arg Ala Tyr Tyr Leu Gly
                    645                 650                 655

    Pro Lys Gly Glu Lys Leu Leu Val Phe Asp Tyr Met Ser Lys Gly Ser
                660                 665                 670

    Leu Ala Ser Phe Leu His Gly Gly Gly Thr Glu Thr Phe Ile Asp Trp
            675                 680                 685

    Pro Thr Arg Met Lys Ile Ala Gln Asp Leu Ala Arg Gly Leu Phe Cys
        690                 695                 700

    Leu His Ser Gln Glu Asn Ile Ile His Gly Asn Leu Thr Ser Ser Asn
    705                 710                 715                 720

    Val Leu Leu Asp Glu Asn Thr Asn Ala Lys Ile Ala Asp Phe Gly Leu
                    725                 730                 735

    Ser Arg Leu Met Ser Thr Ala Ala Asn Ser Asn Val Ile Ala Thr Ala
                740                 745                 750

    Gly Ala Leu Gly Tyr Arg Ala Pro Glu Leu Ser Lys Leu Lys Lys Ala
            755                 760                 765

    Asn Thr Lys Thr Asp Ile Tyr Ser Leu Gly Val Ile Leu Leu Glu Leu
        770                 775                 780

    Leu Thr Arg Lys Ser Pro Gly Val Pro Met Asn Gly Leu Asp Leu Pro
    785                 790                 795                 800

    Gln Trp Val Ala Ser Val Val Lys Glu Glu Trp Thr Asn Glu Val Phe
                    805                 810                 815

    Asp Ala Asp Leu Met Arg Asp Ala Ser Thr Val Gly Asp Glu Leu Leu
                820                 825                 830

    Asn Thr Leu Lys Leu Ala Leu His Cys Val Asp Pro Ser Pro Ser Ala
            835                 840                 845

    Arg Pro Glu Val His Gln Val Leu Gln Gln Leu Glu Glu Ile Arg Pro
        850                 855                 860

    Glu Arg Ser Val Thr Ala Ser Pro Gly Asp Asp Ile Val
    865                 870                 875
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<210>      1113
<211>      854
<212>      PRT
<213>      Glycine max

<223>      Seq ID: rhg1_lee_amplicon

<400>      1113
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Met Val Val Ala Val Glu Lys Thr Asn Leu Thr Ser Gln Ser Gln Cys
1   5   10   15

Phe Asn Arg Val Ser Asp Lys Lys Lys Glu Arg Cys Lys Thr His Met
            20   25   30

Asn Asn Val Asn Pro Cys Cys Phe Leu Phe Leu Leu Cys Val Trp Ser
        35   40   45

Leu Val Val Leu Pro Ser Cys Val Arg Pro Val Leu Cys Glu Asp Glu
    50   55   60

Gly Trp Asp Gly Val Val Val Thr Ala Ser Asn Leu Leu Ala Leu Glu
65   70   75   80

Ala Phe Lys Gln Glu Leu Val Asp Pro Gln Gly Phe Leu Arg Ser Trp
            85   90   95

Asn Asp Ser Gly Tyr Gly Ala Cys Ser Gly Gly Trp Val Gly Ile Lys
            100   105   110

Cys Ala Gln Gly Gln Val Ile Val Ile Gln Leu Pro Trp Lys Gly Leu
        115   120   125

Arg Gly Arg Ile Thr Asp Lys Ile Gly Gln Leu Gln Gly Leu Arg Lys
    130   135   140

Leu Ser Leu His Asp Asn Gln Ile Gly Gly Ser Ile Pro Ser Thr Leu
145   150   155   160

Gly Leu Leu Pro Asn Leu Arg Gly Val Gln Leu Phe Asn Asn Arg Leu
            165   170   175

Thr Gly Ser Ile Pro Leu Ser Leu Gly Phe Cys Pro Leu Leu Gln Ser
        180   185   190

Leu Asp Leu Ser Asn Asn Leu Leu Thr Gly Ala Ile Pro Tyr Ser Leu
    195   200   205

Ala Asn Ser Thr Lys Leu Tyr Trp Leu Asn Leu Ser Phe Asn Ser Phe
    210   215   220

Ser Gly Pro Leu Pro Ala Ser Leu Thr His Ser Phe Ser Leu Thr Phe
225   230   235   240

Leu Ser Leu Gln Asn Asn Asn Leu Ser Gly Ser Leu Pro Asn Ser Trp
            245   250   255

```
Gly Gly Asn Ser Lys Asn Gly Phe Phe Arg Leu Gln Asn Leu Ile Leu
            260                 265                 270

Asp Asn Asn Phe Phe Thr Gly Asp Val Pro Ala Ser Leu Gly Ser Leu
            275                 280                 285

Arg Glu Leu Asn Glu Ile Ser Leu Ser His Asn Lys Phe Ser Gly Ala
    290                 295                 300

Ile Pro Asn Glu Ile Gly Thr Leu Ser Arg Leu Lys Thr Leu Asp Ile
305                 310                 315                 320

Ser Asn Asn Ala Leu Asn Gly Asn Leu Pro Ala Thr Leu Ser Asn Leu
                325                 330                 335

Ser Ser Leu Thr Leu Leu Asn Ala Glu Asn Asn Leu Leu Asp Asn Gln
            340                 345                 350

Ile Pro Gln Ser Leu Gly Arg Leu Arg Asn Leu Ser Val Leu Ile Leu
        355                 360                 365

Ser Arg Asn Gln Phe Ser Gly His Ile Pro Ser Ser Ile Ala Asn Ile
    370                 375                 380

Ser Ser Leu Arg Gln Leu Asp Leu Ser Leu Asn Asn Phe Ser Gly Glu
385                 390                 395                 400

Ile Pro Val Ser Phe Asp Ser Gln Arg Ser Leu Asn Leu Phe Asn Val
            405                 410                 415

Ser Tyr Asn Ser Leu Ser Gly Ser Val Pro Pro Leu Leu Ala Lys Lys
            420                 425                 430

Phe Asn Ser Ser Ser Phe Val Gly Asn Ile Gln Leu Cys Gly Tyr Ser
        435                 440                 445

Pro Ser Thr Pro Cys Leu Ser Gln Ala Pro Ser Gln Gly Val Ile Ala
    450                 455                 460

Pro Pro Pro Glu Val Ser Lys His His His His Arg Lys Leu Ser Thr
465                 470                 475                 480

Lys Asp Ile Ile Leu Ile Val Ala Gly Val Leu Leu Val Val Leu Ile
            485                 490                 495

Ile Leu Cys Cys Val Leu Leu Phe Cys Leu Ile Arg Lys Arg Ser Thr
        500                 505                 510

Ser Lys Ala Gly Asn Gly Gln Ala Thr Glu Gly Arg Ala Ala Thr Met
        515                 520                 525

Arg Thr Glu Lys Gly Val Pro Pro Val Ala Ala Gly Asp Val Glu Ala
    530                 535                 540

Gly Gly Glu Ala Gly Gly Lys Leu Val His Phe Asp Gly Pro Met Ala
545                 550                 555                 560
```

```
Phe Thr Ala Asp Asp Leu Leu Cys Ala Thr Ala Glu Ile Met Gly Lys
                565                   570                   575

Ser Thr Tyr Gly Thr Val Tyr Lys Ala Ile Leu Glu Asp Gly Ser Gln
            580                   585                   590

Val Ala Val Lys Arg Leu Arg Glu Lys Ile Thr Lys Gly His Arg Glu
        595                   600                   605

Phe Glu Ser Glu Val Ser Val Leu Gly Lys Ile Arg His Pro Asn Val
    610                   615                   620

Leu Ala Leu Arg Ala Tyr Tyr Leu Gly Pro Lys Gly Glu Lys Leu Leu
625                   630                   635                   640

Val Phe Asp Tyr Met Ser Lys Gly Ser Leu Ala Ser Phe Leu His Gly
                645                   650                   655

Gly Gly Thr Glu Thr Phe Ile Asp Trp Pro Thr Arg Met Lys Ile Ala
            660                   665                   670

Gln Asp Leu Ala Arg Gly Leu Phe Cys Leu His Ser Gln Glu Asn Ile
        675                   680                   685

Ile His Gly Asn Leu Thr Ser Ser Asn Val Leu Leu Asp Glu Asn Thr
    690                   695                   700

Asn Ala Lys Ile Ala Asp Phe Gly Leu Ser Arg Leu Met Ser Thr Ala
705                   710                   715                   720

Ala Asn Ser Asn Val Ile Ala Thr Ala Gly Ala Leu Gly Tyr Arg Ala
                725                   730                   735

Pro Glu Leu Ser Lys Leu Lys Lys Ala Asn Thr Lys Thr Asp Ile Tyr
            740                   745                   750

Ser Leu Gly Val Ile Leu Leu Glu Leu Leu Thr Arg Lys Ser Pro Gly
        755                   760                   765

Val Pro Met Asn Gly Leu Asp Leu Pro Gln Trp Val Ala Ser Val Val
    770                   775                   780

Lys Glu Glu Trp Thr Asn Glu Val Phe Asp Ala Asp Leu Met Arg Asp
785                   790                   795                   800

Ala Ser Thr Val Gly Asp Glu Leu Leu Asn Thr Leu Lys Leu Ala Leu
                805                   810                   815

His Cys Val Asp Pro Ser Pro Ser Ala Arg Pro Glu Val His Gln Val
            820                   825                   830

Leu Gln Gln Leu Glu Glu Ile Arg Pro Glu Arg Ser Val Thr Ala Ser
        835                   840                   845

Pro Gly Asp Asp Ile Val
    850
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<210>      1114
<211>      877
<212>      PRT
<213>      Glycine max

<223>      Seq ID: rhg1_pi200499_amplicon

<400>      1114
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Met Asp Ala Cys Gly Met Ser Ser Ser Asn Ser Lys His Val Val Asp
1   5   10   15

Gln Lys Arg Ser Thr Met Asn Met Met Ile Thr Thr Ile Leu Leu Arg
            20   25   30

Phe Trp Asp Arg Tyr Asp Met Asn Cys Asp Tyr Thr Thr Asn Ser Tyr
        35   40   45

Glu Pro Gly Thr Gln Leu Ala Pro Ser Ser Pro Arg Asp Thr Ser Val
    50   55   60

Lys Leu Gly Asp Ala Ser Ser Leu Val Val Leu Pro Ser Cys Val Arg
65   70   75   80

Pro Val Leu Cys Glu Asp Glu Gly Trp Asp Gly Val Val Val Thr Ala
                85   90   95

Ser Asn Leu Leu Ala Leu Glu Ala Phe Lys Gln Glu Leu Val Asp Pro
            100   105   110

Glu Gly Phe Leu Arg Ser Trp Asn Asp Ser Gly Tyr Gly Ala Cys Ser
        115   120   125

Gly Gly Trp Val Gly Ile Lys Cys Ala Gln Gly Gln Val Ile Val Ile
    130   135   140

Gln Leu Pro Trp Lys Gly Leu Arg Gly Arg Ile Thr Asp Lys Ile Gly
145   150   155   160

Gln Leu Gln Gly Leu Arg Lys Leu Ser Leu His Asp Asn Gln Ile Gly
            165   170   175

Gly Ser Ile Pro Ser Thr Leu Gly Leu Leu Pro Asn Leu Arg Gly Val
            180   185   190

Gln Leu Phe Asn Asn Arg Leu Thr Gly Ser Ile Pro Leu Ser Leu Gly
        195   200   205

Phe Cys Pro Leu Leu Gln Ser Leu Asp Leu Ser Asn Asn Leu Leu Thr
    210   215   220

Gly Ala Ile Pro Tyr Ser Leu Ala Asn Ser Thr Lys Leu Tyr Trp Leu
225   230   235   240

Asn Leu Ser Phe Asn Ser Phe Ser Gly Pro Leu Pro Ala Ser Leu Thr
            245   250   255

His Ser Phe Ser Leu Thr Phe Leu Ser Leu Gln Asn Asn Asn Leu Ser
          260   265   270

Gly Ser Leu Pro Asn Ser Trp Gly Gly Asn Ser Lys Asn Gly Phe Phe
          275   280   285

Arg Leu Gln Asn Leu Ile Leu Asp Asn Asn Phe Phe Thr Gly Asp Val
      290   295   300

Pro Ala Ser Leu Gly Ser Leu Arg Glu Leu Asn Glu Ile Ser Leu Ser
305   310   315   320

His Asn Lys Phe Ser Gly Ala Ile Pro Asn Glu Ile Gly Thr Leu Ser
              325   330   335

Arg Leu Lys Thr Leu Asp Ile Ser Asn Asn Ala Leu Asn Gly Asn Leu
          340   345   350

Pro Ala Thr Leu Ser Asn Leu Ser Ser Leu Thr Leu Leu Asn Ala Glu
          355   360   365

Asn Asn Leu Leu Asp Asn Gln Ile Pro Gln Ser Leu Gly Arg Leu Arg
      370   375   380

Asn Leu Ser Val Leu Ile Leu Ser Arg Asn Gln Phe Ser Gly His Ile
385   390   395   400

Pro Ser Ser Ile Ala Asn Ile Ser Ser Leu Arg Gln Leu Asp Leu Ser
              405   410   415

Leu Asn Asn Phe Ser Gly Glu Ile Pro Val Ser Phe Asp Ser Gln Arg
          420   425   430

Ser Leu Asn Leu Phe Asn Val Ser Tyr Asn Ser Leu Ser Gly Ser Val
          435   440   445

Pro Pro Leu Leu Ala Lys Lys Phe Asn Ser Ser Ser Phe Val Gly Asn
      450   455   460

Ile Gln Leu Cys Gly Tyr Ser Pro Ser Thr Pro Cys Leu Ser Gln Ala
465   470   475   480

Pro Ser Gln Gly Val Ile Ala Pro Pro Glu Val Ser Lys His His
              485   490   495

His His Arg Lys Leu Ser Thr Lys Asp Ile Ile Leu Ile Val Ala Gly
          500   505   510

Val Leu Leu Val Val Leu Ile Ile Leu Cys Cys Val Leu Leu Phe Cys
          515   520   525

Leu Ile Arg Lys Arg Ser Thr Ser Lys Ala Gly Asn Gly Gln Ala Thr
          530   535   540

Glu Gly Arg Ala Ala Thr Met Arg Thr Glu Lys Gly Val Pro Pro Val
545   550   555   560

Ala Ala Gly Asp Val Glu Ala Gly Gly Glu Ala Gly Gly Lys Leu Val

                    565   570   575

    His Phe Asp Gly Pro Met Ala Phe Thr Ala Asp Asp Leu Leu Cys Ala
                580   585   590

    Thr Ala Glu Ile Met Gly Lys Ser Thr Tyr Gly Thr Val Tyr Lys Ala
             595   600   605

    Ile Leu Glu Asp Gly Ser Gln Val Ala Val Lys Arg Leu Arg Glu Lys
         610   615   620

    Ile Thr Lys Gly His Arg Glu Phe Glu Ser Glu Val Ser Val Leu Gly
    625   630   635   640

    Lys Ile Arg His Pro Asn Val Leu Ala Leu Arg Ala Tyr Tyr Leu Gly
                      645   650   655

    Pro Lys Gly Glu Lys Leu Leu Val Phe Asp Tyr Met Ser Lys Gly Ser
                660   665   670

    Leu Ala Ser Phe Leu His Gly Gly Gly Thr Glu Thr Phe Ile Asp Trp
             675   680   685

    Pro Thr Arg Met Lys Ile Ala Gln Asp Leu Ala Arg Gly Leu Phe Cys
         690   695   700

    Leu His Ser Gln Glu Asn Ile Ile His Gly Asn Leu Thr Ser Ser Asn
    705   710   715   720

    Val Leu Leu Asp Glu Asn Thr Asn Ala Lys Ile Ala Asp Phe Gly Leu
                   ·725   730   735

    Ser Arg Leu Met Ser Thr Ala Ala Asn Ser Asn Val Ile Ala Thr Ala
                740   745   750

    Gly Ala Leu Gly Tyr Arg Ala Pro Glu Leu Ser Lys Leu Lys Lys Ala
             755   760   765

    Asn Thr Lys Thr Asp Ile Tyr Ser Leu Gly Val Ile Leu Leu Glu Leu
         770   775   780

    Leu Thr Arg Lys Ser Pro Gly Val Pro Met Asn Gly Leu Asp Leu Pro
    785   790   795   800

    Gln Trp Val Ala Ser Val Val Lys Glu Glu Trp Thr Asn Glu Val Phe
                805   810   815

    Asp Ala Asp Leu Met Arg Asp Ala Ser Thr Val Gly Asp Glu Leu Leu
             820   825   830

    Asn Thr Leu Lys Leu Ala Leu His Cys Val Asp Pro Ser Pro Ser Ala
             835   840   845

    Arg Pro Glu Val His Gln Val Leu Gln Gln Leu Glu Glu Ile Arg Pro
         850   855   860

    Glu Arg Ser Val Thr Ala Ser Pro Gly Asp Asp Ile Val
    865   870   875

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<210>      1115
<211>      854
<212>      PRT
<213>      Glycine max

<223>      Seq ID: rhg1_pi200499_amplicon

<400>      1115
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Met Val Val Ala Val Glu Lys Thr Asn Leu Thr Ser Gln Ser Gln Cys
1   5   10   15

Phe Asn Arg Val Ser Asp Lys Lys Lys Glu Arg Cys Lys Thr His Met
            20   25   30

Asn Asn Val Asn Pro Cys Cys Phe Leu Phe Leu Leu Cys Val Trp Ser
        35   40   45

Leu Val Val Leu Pro Ser Cys Val Arg Pro Val Leu Cys Glu Asp Glu
    50   55   60

Gly Trp Asp Gly Val Val Val Thr Ala Ser Asn Leu Leu Ala Leu Glu
65   70   75   80

Ala Phe Lys Gln Glu Leu Val Asp Pro Gln Gly Phe Leu Arg Ser Trp
            85   90   95

Asn Asp Ser Gly Tyr Gly Ala Cys Ser Gly Gly Trp Val Gly Ile Lys
            100   105   110

Cys Ala Gln Gly Gln Val Ile Val Ile Gln Leu Pro Trp Lys Gly Leu
        115   120   125

Arg Gly Arg Ile Thr Asp Lys Ile Gly Gln Leu Gln Gly Leu Arg Lys
    130   135   140

Leu Ser Leu His Asp Asn Gln Ile Gly Gly Ser Ile Pro Ser Thr Leu
145   150   155   160

Gly Leu Leu Pro Asn Leu Arg Gly Val Gln Leu Phe Asn Asn Arg Leu
            165   170   175

Thr Gly Ser Ile Pro Leu Ser Leu Gly Phe Cys Pro Leu Leu Gln Ser
            180   185   190

Leu Asp Leu Ser Asn Asn Leu Leu Thr Gly Ala Ile Pro Tyr Ser Leu
    195   200   205

Ala Asn Ser Thr Lys Leu Tyr Trp Leu Asn Leu Ser Phe Asn Ser Phe
    210   215   220

Ser Gly Pro Leu Pro Ala Ser Leu Thr His Ser Phe Ser Leu Thr Phe
225   230   235   240

Leu Ser Leu Gln Asn Asn Asn Leu Ser Gly Ser Leu Pro Asn Ser Trp
            245   250   255

```
Gly Gly Asn Ser Lys Asn Gly Phe Phe Arg Leu Gln Asn Leu Ile Leu
            260                 265                 270

Asp Asn Asn Phe Phe Thr Gly Asp Val Pro Ala Ser Leu Gly Ser Leu
        275                 280                 285

Arg Glu Leu Asn Glu Ile Ser Leu Ser His Asn Lys Phe Ser Gly Ala
    290                 295                 300

Ile Pro Asn Glu Ile Gly Thr Leu Ser Arg Leu Lys Thr Leu Asp Ile
305                 310                 315                 320

Ser Asn Asn Ala Leu Asn Gly Asn Leu Pro Ala Thr Leu Ser Asn Leu
                325                 330                 335

Ser Ser Leu Thr Leu Leu Asn Ala Glu Asn Asn Leu Leu Asp Asn Gln
                340                 345                 350

Ile Pro Gln Ser Leu Gly Arg Leu Arg Asn Leu Ser Val Leu Ile Leu
        355                 360                 365

Ser Arg Asn Gln Phe Ser Gly His Ile Pro Ser Ser Ile Ala Asn Ile
    370                 375                 380

Ser Ser Leu Arg Gln Leu Asp Leu Ser Leu Asn Asn Phe Ser Gly Glu
385                 390                 395                 400

Ile Pro Val Ser Phe Asp Ser Gln Arg Ser Leu Asn Leu Phe Asn Val
                405                 410                 415

Ser Tyr Asn Ser Leu Ser Gly Ser Val Pro Pro Leu Leu Ala Lys Lys
            420                 425                 430

Phe Asn Ser Ser Ser Phe Val Gly Asn Ile Gln Leu Cys Gly Tyr Ser
        435                 440                 445

Pro Ser Thr Pro Cys Leu Ser Gln Ala Pro Ser Gln Gly Val Ile Ala
    450                 455                 460

Pro Pro Pro Glu Val Ser Lys His His His Arg Lys Leu Ser Thr
465                 470                 475                 480

Lys Asp Ile Ile Leu Ile Val Ala Gly Val Leu Leu Val Val Leu Ile
                485                 490                 495

Ile Leu Cys Cys Val Leu Phe Cys Leu Ile Arg Lys Arg Ser Thr
            500                 505                 510

Ser Lys Ala Gly Asn Gly Gln Ala Thr Glu Gly Arg Ala Ala Thr Met
    515                 520                 525

Arg Thr Glu Lys Gly Val Pro Pro Val Ala Ala Gly Asp Val Glu Ala
    530                 535                 540

Gly Gly Glu Ala Gly Gly Lys Leu Val His Phe Asp Gly Pro Met Ala
545                 550                 555                 560
```

Phe Thr Ala Asp Asp Leu Leu Cys Ala Thr Ala Glu Ile Met Gly Lys
               565   570   575

Ser Thr Tyr Gly Thr Val Tyr Lys Ala Ile Leu Glu Asp Gly Ser Gln
           580   585   590

Val Ala Val Lys Arg Leu Arg Glu Lys Ile Thr Lys Gly His Arg Glu
       595   600   605

Phe Glu Ser Glu Val Ser Val Leu Gly Lys Ile Arg His Pro Asn Val
   610   615   620

Leu Ala Leu Arg Ala Tyr Tyr Leu Gly Pro Lys Gly Glu Lys Leu Leu
625   630   635   640

Val Phe Asp Tyr Met Ser Lys Gly Ser Leu Ala Ser Phe Leu His Gly
               645   650   655

Gly Gly Thr Glu Thr Phe Ile Asp Trp Pro Thr Arg Met Lys Ile Ala
           660   665   670

Gln Asp Leu Ala Arg Gly Leu Phe Cys Leu His Ser Gln Glu Asn Ile
       675   680   685

Ile His Gly Asn Leu Thr Ser Ser Asn Val Leu Leu Asp Glu Asn Thr
   690   695   700

Asn Ala Lys Ile Ala Asp Phe Gly Leu Ser Arg Leu Met Ser Thr Ala
705   710   715   720

Ala Asn Ser Asn Val Ile Ala Thr Ala Gly Ala Leu Gly Tyr Arg Ala
           725   730   735

Pro Glu Leu Ser Lys Leu Lys Lys Ala Asn Thr Lys Thr Asp Ile Tyr
           740   745   750

Ser Leu Gly Val Ile Leu Leu Glu Leu Leu Thr Arg Lys Ser Pro Gly
       755   760   765

Val Pro Met Asn Gly Leu Asp Leu Pro Gln Trp Val Ala Ser Val Val
   770   775   780

Lys Glu Glu Trp Thr Asn Glu Val Phe Asp Ala Asp Leu Met Arg Asp
785   790   795   800

Ala Ser Thr Val Gly Asp Glu Leu Leu Asn Thr Leu Lys Leu Ala Leu
           805   810   815

His Cys Val Asp Pro Ser Pro Ser Ala Arg Pro Glu Val His Gln Val
       820   825   830

Leu Gln Gln Leu Glu Glu Ile Arg Pro Glu Arg Ser Val Thr Ala Ser
       835   840   845

Pro Gly Asp Asp Ile Val
   850

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<211>      894
<212>      PRT
<213>      Glycine max

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<400>      1116
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Met Ser Asn Phe Leu Lys Ser Leu Thr Pro Pro Pro Ser Gly Trp Ser
1   5   10   15

Glu Thr Thr Pro Phe Cys Gln Trp Lys Gly Ile Gln Cys Asp Ser Ser
                20   25   30

Ser His Val Thr Ser Ile Ser Leu Ala Ser His Ser Leu Thr Gly Thr
            35   40   45

Leu Pro Ser Asp Leu Asn Ser Leu Ser Gln Leu Arg Thr Leu Ser Leu
        50   55   60

Gln Asp Asn Ser Leu Thr Gly Thr Leu Pro Ser Leu Ser Asn Leu Ser
65   70   75   80

Phe Leu Gln Thr Val Tyr Leu Asn Arg Asn Asn Phe Ser Ser Val Ser
                85   90   95

Pro Thr Ala Phe Ala Ser Leu Thr Ser Leu Gln Thr Leu Ser Leu Gly
            100   105   110

Ser Asn Pro Ala Leu Gln Pro Trp Ser Phe Pro Thr Asp Leu Thr Ser
        115   120   125

Ser Ser Asn Leu Ile Asp Leu Asp Leu Ala Thr Val Ser Leu Thr Gly
130   135   140

Pro Leu Pro Asp Ile Phe Asp Lys Phe Pro Ser Leu Gln His Leu Arg
145   150   155   160

Leu Ser Tyr Asn Asn Leu Thr Gly Asn Leu Pro Ser Ser Phe Ser Ala
                165   170   175

Ala Asn Asn Leu Glu Thr Leu Trp Leu Asn Asn Gln Ala Ala Gly Leu
            180   185   .   190

Ser Gly Thr Leu Leu Val Leu Ser Asn Met Ser Ala Leu Asn Gln Ser
        195   200   205

Trp Leu Asn Lys Asn Gln Phe Thr Gly Ser Ile Pro Asp Leu Ser Gln
    210   215   220

Cys Thr Ala Leu Ser Asp Leu Gln Leu Arg Asp Asn Gln Leu Thr Gly
225   230   235   240

Val Val Pro Ala Ser Leu Thr Ser Leu Pro Ser Leu Lys Lys Val Ser
                245   250   255

Leu Asp Asn Asn Glu Leu Gln Gly Pro Val Pro Val Phe Gly Lys Gly

```
                 260                    265                    270

Val Asn Val Thr Leu Asp Gly Ile Asn Ser Phe Cys Leu Asp Thr Pro
         275                    280                    285

Gly Asn Cys Asp Pro Arg Val Met Val Leu Leu Gln Ile Ala Glu Ala
     290                    295                    300

Phe Gly Tyr Pro Ile Arg Leu Ala Glu Ser Trp Lys Gly Asn Asp Pro
305                    310                    315                    320

Cys Asp Gly Trp Asn Tyr Val Val Cys Ala Ala Gly Lys Ile Ile Thr
                 325                    330                    335

Val Asn Phe Glu Lys Gln Gly Leu Gln Gly Thr Ile Ser Pro Ala Phe
         340                    345                    350

Ala Asn Leu Thr Asp Leu Arg Thr Leu Phe Leu Asn Gly Asn Asn Leu
         355                    360                    365

Ile Gly Ser Ile Pro Asp Ser Leu Ile Thr Leu Pro Gln Leu Gln Thr
     370                    375                    380

Leu Asp Val Ser Asp Asn Asn Leu Ser Gly Leu Val Pro Lys Phe Pro
385                    390                    395                    400

Pro Lys Val Lys Leu Val Thr Ala Gly Asn Ala Leu Leu Gly Lys Pro
                 405                    410                    415

Leu Ser Pro Gly Gly Gly Pro Ser Gly Thr Thr Pro Ser Gly Ser Ser
         420                    425                    430

Thr Gly Gly Ser Gly Gly Glu Ser Ser Lys Gly Asn Ser Ser Val Ser
         435                    440                    445

Pro Gly Trp Ile Ala Gly Ile Val Val Ile Val Leu Phe Phe Ile Ala
     450                    455                    460

Val Val Leu Phe Val Ser Trp Lys Cys Phe Val Asn Lys Leu Gln Gly
465                    470                    475                    480

Lys Phe Ser Arg Val Lys Gly His Glu Asn Gly Lys Gly Gly Phe Lys
                 485                    490                    495

Leu Asp Ala Val His Val Ser Asn Gly Tyr Gly Gly Val Pro Val Glu
         500                    505                    510

Leu Gln Ser Gln Ser Ser Gly Asp Arg Ser Asp Leu His Ala Leu Asp
         515                    520                    525

Gly Pro Thr Phe Ser Ile Gln Val Leu Arg Gln Val Thr Asn Asn Phe
     530                    535                    540

Ser Glu Glu Asn Ile Leu Gly Arg Gly Gly Phe Gly Val Val Tyr Lys
545                    550                    555                    560

Gly Val Leu His Asp Gly Thr Lys Ile Ala Val Lys Arg Met Glu Ser
                 565                    570                    575
```

```
Val Ala Met Gly Asn Lys Gly Gln Lys Glu Phe Glu Ala Glu Ile Ala
            580                 585                 590

Leu Leu Ser Lys Val Arg His Arg His Leu Val Ala Leu Leu Gly Tyr
            595                 600                 605

Cys Ile Asn Gly Asn Glu Arg Leu Leu Val Tyr Glu Tyr Met Pro Gln
    610                 615                 620

Gly Thr Leu Thr Gln His Leu Phe Glu Trp Gln Glu His Gly Tyr Ala
625                 630                 635                 640

Pro Leu Thr Trp Lys Gln Arg Val Val Ile Ala Leu Asp Val Ala Arg
                645                 650                 655

Gly Val Glu Tyr Leu His Ser Leu Ala Gln Gln Ser Phe Ile His Arg
            660                 665                 670

Asp Leu Lys Pro Ser Asn Ile Leu Leu Gly Asp Asp Met Arg Ala Lys
        675                 680                 685

Val Ala Asp Phe Gly Leu Val Lys Asn Ala Pro Asp Gly Lys Tyr Ser
    690                 695                 700

Val Glu Thr Arg Leu Ala Gly Thr Phe Gly Tyr Leu Ala Pro Glu Tyr
705                 710                 715                 720

Ala Ala Thr Gly Arg Val Thr Thr Lys Val Asp Val Tyr Ala Phe Gly
                725                 730                 735

Val Val Leu Met Glu Leu Ile Thr Gly Arg Lys Ala Leu Asp Asp Thr
            740                 745                 750

Val Pro Asp Glu Arg Ser His Leu Val Thr Trp Phe Arg Arg Val Leu
            755                 760                 765

Ile Asn Lys Glu Asn Ile Pro Lys Ala Ile Asp Gln Ile Leu Asn Pro
    770                 775                 780

Asp Glu Glu Thr Met Gly Ser Ile Tyr Thr Val Ala Glu Leu Ala Gly
785                 790                 795                 800

His Cys Thr Ala Arg Glu Pro Tyr Gln Arg Pro Asp Met Gly His Ala
                805                 810                 815

Val Asn Val Leu Val Pro Leu Val Glu Gln Trp Lys Pro Thr Ser His
            820                 825                 830

Asp Glu Glu Glu Asp Gly Ser Gly Gly Asp Leu His Met Ser Leu
        835                 840                 845

Pro Gln Ala Leu Arg Arg Trp Gln Ala Asn Glu Gly Thr Ser Ser Ile
    850                 855                 860

Phe Asn Asp Ile Ser Ile Ser Gln Thr Gln Ser Ser Ile Ser Ser Lys
865                 870                 875                 880
```

```
Pro Ala Gly Phe Ala Asp Ser Phe Asp Ser Met Asp Cys Arg
                885                       890


<210>     1117
<211>     894
<212>     PRT
<213>     Glycine max

<223>     Seq ID: rhg4_Minsoy_amplicon

<400>     1117

Met Ser Asn Phe Leu Lys Ser Leu Thr Pro Pro Pro Ser Gly Trp Ser
1                   5                   10                  15

Glu Thr Thr Pro Phe Cys Gln Trp Lys Gly Ile Gln Cys Asp Ser Ser
                20                  25                  30

Ser His Val Thr Ser Ile Ser Leu Ala Ser His Ser Leu Thr Gly Thr
            35                  40                  45

Leu Pro Ser Asp Leu Asn Ser Leu Ser Gln Leu Arg Thr Leu Ser Leu
        50                  55                  60

Gln Asp Asn Ser Leu Thr Gly Thr Leu Pro Ser Leu Ser Asn Leu Ser
65                  70                  75                  80

Phe Leu Gln Thr Val Tyr Leu Asn Arg Asn Asn Phe Ser Ser Val Ser
                85                  90                  95

Pro Thr Ala Phe Ala Ser Leu Thr Ser Leu Gln Thr Leu Ser Leu Gly
            100                 105                 110

Ser Asn Pro Ala Leu Gln Pro Trp Ser Phe Pro Thr Asp Leu Thr Ser
        115                 120                 125

Ser Ser Asn Leu Ile Asp Leu Asp Leu Ala Thr Val Ser Leu Thr Gly
    130                 135                 140

Pro Leu Pro Asp Ile Phe Asp Lys Phe Pro Ser Leu Gln His Leu Arg
145                 150                 155                 160

Leu Ser Tyr Asn Asn Leu Thr Gly Asn Leu Pro Ser Ser Phe Ser Ala
                165                 170                 175

Ala Asn Asn Leu Glu Thr Leu Trp Leu Asn Asn Gln Ala Ala Gly Leu
            180                 185                 190

Ser Gly Thr Leu Leu Val Leu Ser Asn Met Ser Ala Leu Asn Gln Ser
        195                 200                 205

Trp Leu Asn Lys Asn Gln Phe Thr Gly Ser Ile Pro Asp Leu Ser Gln
    210                 215                 220

Cys Thr Ala Leu Ser Asp Leu Gln Leu Arg Asp Asn Gln Leu Thr Gly
225                 230                 235                 240
```

```
Val Val Pro Ala Ser Leu Thr Ser Leu Pro Ser Leu Lys Lys Val Ser
                245                 250                 255

Leu Asp Asn Asn Glu Leu Gln Gly Pro Val Pro Val Phe Gly Lys Gly
            260                 265                 270

Val Asn Val Thr Leu Asp Gly Ile Asn Ser Phe Cys Leu Asp Thr Pro
            275                 280                 285

Gly Asn Cys Asp Pro Arg Val Met Val Leu Leu Gln Ile Ala Glu Ala
        290                 295                 300

Phe Gly Tyr Pro Ile Arg Leu Ala Glu Ser Trp Lys Gly Asn Asp Pro
305                 310                 315                 320

Cys Asp Gly Trp Asn Tyr Val Val Cys Ala Ala Gly Lys Ile Ile Thr
                325                 330                 335

Val Asn Phe Glu Lys Gln Gly Leu Gln Gly Thr Ile Ser Pro Ala Phe
            340                 345                 350

Ala Asn Leu Thr Asp Leu Arg Thr Leu Phe Leu Asn Gly Asn Asn Leu
            355                 360                 365

Ile Gly Ser Ile Pro Asp Ser Leu Ile Thr Leu Pro Gln Leu Gln Thr
        370                 375                 380

Leu Asp Val Ser Asp Asn Asn Leu Ser Gly Leu Val Pro Lys Phe Pro
385                 390                 395                 400

Pro Lys Val Lys Leu Val Thr Ala Gly Asn Ala Leu Leu Gly Lys Pro
                405                 410                 415

Leu Ser Pro Gly Gly Pro Ser Gly Thr Thr Pro Ser Gly Ser Ser
            420                 425                 430

Thr Gly Gly Ser Gly Gly Glu Ser Ser Lys Gly Asn Ser Ser Val Ser
        435                 440                 445

Pro Gly Trp Ile Ala Gly Ile Val Val Ile Val Leu Phe Phe Ile Ala
        450                 455                 460

Val Val Leu Phe Val Ser Trp Lys Cys Phe Val Asn Lys Leu Gln Gly
465                 470                 475                 480

Lys Phe Ser Arg Val Lys Gly His Glu Asn Gly Lys Gly Gly Phe Lys
                485                 490                 495

Leu Asp Ala Val His Val Ser Asn Gly Tyr Gly Gly Val Pro Val Glu
            500                 505                 510

Leu Gln Ser Gln Ser Ser Gly Asp Arg Ser Asp Leu His Ala Leu Asp
            515                 520                 525

Gly Pro Thr Phe Ser Ile Gln Val Leu Arg Gln Val Thr Asn Asn Phe
        530                 535                 540

Ser Glu Glu Asn Ile Leu Gly Arg Gly Gly Phe Gly Val Val Tyr Lys
```

```
    545                    550                    555                    560

Gly Val Leu His Asp Gly Thr Lys Ile Ala Val Lys Arg Met Glu Ser
                   565                    570                    575

Val Ala Met Gly Asn Lys Gly Gln Lys Glu Phe Glu Ala Glu Ile Ala
              580                    585                    590

Leu Leu Ser Lys Val Arg His Arg His Leu Val Ala Leu Leu Gly Tyr
         595                    600                    605

Cys Ile Asn Gly Asn Glu Arg Leu Leu Val Tyr Glu Tyr Met Pro Gln
    610                    615                    620

Gly Thr Leu Thr Gln His Leu Phe Glu Trp Gln Glu His Gly Tyr Ala
625                    630                    635                    640

Pro Leu Thr Trp Lys Gln Arg Val Val Ile Ala Leu Asp Val Ala Arg
                   645                    650                    655

Gly Val Glu Tyr Leu His Ser Leu Ala Gln Gln Ser Phe Ile His Arg
              660                    665                    670

Asp Leu Lys Pro Ser Asn Ile Leu Leu Gly Asp Asp Met Arg Ala Lys
              675                    680                    685

Val Ala Asp Phe Gly Leu Val Lys Asn Ala Pro Asp Gly Lys Tyr Ser
    690                    695                    700

Val Glu Thr Arg Leu Ala Gly Thr Phe Gly Tyr Leu Ala Pro Glu Tyr
705                    710                    715                    720

Ala Ala Thr Gly Arg Val Thr Thr Lys Val Asp Val Tyr Ala Phe Gly
                   725                    730                    735

Val Val Leu Met Glu Leu Ile Thr Gly Arg Lys Ala Leu Asp Asp Thr
              740                    745                    750

Val Pro Asp Glu Arg Ser His Leu Val Thr Trp Phe Arg Arg Val Leu
         755                    760                    765

Ile Asn Lys Glu Asn Ile Pro Lys Ala Ile Asp Gln Ile Leu Asn Pro
    770                    775                    780

Asp Glu Glu Thr Met Gly Ser Ile Tyr Thr Val Ala Glu Leu Ala Gly
785                    790                    795                    800

His Cys Thr Ala Arg Glu Pro Tyr Gln Arg Pro Asp Met Gly His Ala
              805                    810                    815

Val Asn Val Leu Val Pro Leu Val Glu Gln Trp Lys Pro Thr Ser His
         820                    825                    830

Asp Glu Glu Glu Glu Asp Gly Ser Gly Gly Asp Leu His Met Ser Leu
         835                    840                    845

Pro Gln Ala Leu Arg Arg Trp Gln Ala Asn Glu Gly Thr Ser Ser Ile
    850                    855                    860
```

```
Phe Asn Asp Ile Ser Ile Ser Gln Thr Gln Ser Ser Ile Ser Ser Lys
865                 870                 875                 880

Pro Ala Gly Phe Ala Asp Ser Phe Asp Ser Met Asp Cys Arg
                885                 890


<210>     1118
<211>     894
<212>     PRT
<213>     Glycine max

<223>     Seq ID: rhg4_Jack_amplicon

<400>     1118

Met Ser Asn Phe Leu Lys Ser Leu Thr Pro Pro Pro Ser Gly Trp Ser
1                 5                   10                  15

Glu Thr Thr Pro Phe Cys Gln Trp Lys Gly Ile Gln Cys Asp Ser Ser
                20                  25                  30

Ser His Val Thr Ser Ile Ser Leu Ala Ser Gln Ser Leu Thr Gly Thr
        35                  40                  45

Leu Pro Ser Asp Leu Asn Ser Leu Ser Gln Leu Arg Thr Leu Ser Leu
    50                  55                  60

Gln Asp Asn Ser Leu Thr Gly Thr Leu Pro Ser Leu Ser Asn Leu Ser
65                  70                  75                  80

Phe Leu Gln Thr Val Tyr Leu Asn Arg Asn Asn Phe Ser Ser Val Ser
                85                  90                  95

Pro Thr Ala Phe Ala Ser Leu Thr Ser Leu Gln Thr Leu Ser Leu Gly
            100                 105                 110

Ser Asn Pro Ala Leu Gln Pro Trp Ser Phe Pro Thr Asp Leu Thr Ser
        115                 120                 125

Ser Ser Asn Leu Ile Asp Leu Asp Leu Ala Thr Val Ser Leu Thr Gly
    130                 135                 140

Pro Leu Pro Asp Ile Phe Asp Lys Phe Pro Ser Leu Gln His Leu Arg
145                 150                 155                 160

Leu Ser Tyr Asn Asn Leu Thr Gly Asn Leu Pro Ser Ser Phe Ser Ala
                165                 170                 175

Ala Asn Asn Leu Glu Thr Leu Trp Leu Asn Asn Gln Ala Ala Gly Leu
            180                 185                 190

Ser Gly Thr Leu Leu Val Leu Ser Asn Met Ser Ala Leu Asn Gln Ser
        195                 200                 205

Trp Leu Asn Lys Asn Gln Phe Thr Gly Ser Ile Pro Asp Leu Ser Gln
    210                 215                 220
```

```
Cys Thr Ala Leu Ser Asp Leu Gln Leu Arg Asp Asn Gln Leu Thr Gly
225                 230                 235                 240

Val Val Pro Ala Ser Leu Thr Ser Leu Pro Ser Leu Lys Lys Val Ser
                245                 250                 255

Leu Asp Asn Asn Glu Leu Gln Gly Pro Val Pro Val Phe Gly Lys Gly
            260                 265                 270

Val Asn Val Thr Leu Asp Gly Ile Asn Ser Phe Cys Leu Asp Thr Pro
        275                 280                 285

Gly Asn Cys Asp Pro Arg Val Met Val Leu Leu Gln Ile Ala Glu Ala
    290                 295                 300

Phe Gly Tyr Pro Ile Arg Leu Ala Glu Ser Trp Lys Gly Asn Asp Pro
305                 310                 315                 320

Cys Asp Gly Trp Asn Tyr Val Val Cys Ala Ala Gly Lys Ile Ile Thr
                325                 330                 335

Val Asn Phe Glu Lys Gln Gly Leu Gln Gly Thr Ile Ser Pro Ala Phe
            340                 345                 350

Ala Asn Leu Thr Asp Leu Arg Thr Leu Phe Leu Asn Gly Asn Asn Leu
        355                 360                 365

Ile Gly Ser Ile Pro Asp Ser Leu Ile Thr Leu Pro Gln Leu Gln Thr
    370                 375                 380

Leu Asp Val Ser Asp Asn Asn Leu Ser Gly Leu Val Pro Lys Phe Pro
385                 390                 395                 400

Pro Lys Val Lys Leu Val Thr Ala Gly Asn Ala Leu Leu Gly Lys Pro
                405                 410                 415

Leu Ser Pro Gly Gly Gly Pro Ser Gly Thr Thr Pro Ser Gly Ser Ser
            420                 425                 430

Thr Gly Gly Ser Gly Gly Glu Ser Ser Lys Gly Asn Ser Ser Val Ser
        435                 440                 445

Pro Gly Trp Ile Ala Gly Ile Val Val Ile Val Leu Phe Phe Ile Ala
    450                 455                 460

Val Val Leu Phe Val Ser Trp Lys Cys Phe Val Asn Lys Leu Gln Gly
465                 470                 475                 480

Lys Phe Ser Arg Val Lys Gly His Glu Asn Gly Lys Gly Gly Phe Lys
                485                 490                 495

Leu Asp Ala Val His Val Ser Asn Gly Tyr Gly Val Pro Val Glu
            500                 505                 510

Leu Gln Ser Gln Ser Ser Gly Asp Arg Ser Asp Leu His Ala Leu Asp
        515                 520                 525
```

```
Gly Pro Thr Phe Ser Ile Gln Val Leu Arg Gln Val Thr Asn Asn Phe
    530                 535                 540

Ser Glu Glu Asn Ile Leu Gly Arg Gly Gly Phe Gly Val Val Tyr Lys
545                 550                 555                 560

Gly Val Leu His Asp Gly Thr Lys Ile Ala Val Lys Arg Met Glu Ser
                565                 570                 575

Val Ala Met Gly Asn Lys Gly Gln Lys Glu Phe Glu Ala Glu Ile Ala
                580                 585                 590

Leu Leu Ser Lys Val Arg His Arg His Leu Val Ala Leu Leu Gly Tyr
            595                 600                 605

Cys Ile Asn Gly Asn Glu Arg Leu Leu Val Tyr Glu Tyr Met Pro Gln
    610                 615                 620

Gly Thr Leu Thr Gln His Leu Phe Glu Trp Gln Glu His Gly Tyr Ala
625                 630                 635                 640

Pro Leu Thr Trp Lys Gln Arg Val Val Ile Ala Leu Asp Val Ala Arg
                645                 650                 655

Gly Val Glu Tyr Leu His Ser Leu Ala Gln Gln Ser Phe Ile His Arg
                660                 665                 670

Asp Leu Lys Pro Ser Asn Ile Leu Leu Gly Asp Asp Met Arg Ala Lys
            675                 680                 685

Val Ala Asp Phe Gly Leu Val Lys Asn Ala Pro Asp Gly Lys Tyr Ser
    690                 695                 700

Val Glu Thr Arg Leu Ala Gly Thr Phe Gly Tyr Leu Ala Pro Glu Tyr
705                 710                 715                 720

Ala Ala Thr Gly Arg Val Thr Thr Lys Val Asp Val Tyr Ala Phe Gly
                725                 730                 735

Val Val Leu Met Glu Leu Ile Thr Gly Arg Lys Ala Leu Asp Asp Thr
            740                 745                 750

Val Pro Asp Glu Arg Ser His Leu Val Thr Trp Phe Arg Arg Val Leu
            755                 760                 765

Ile Asn Lys Glu Asn Ile Pro Lys Ala Ile Asp Gln Ile Leu Asn Pro
    770                 775                 780

Asp Glu Glu Thr Met Gly Ser Ile Tyr Thr Val Ala Glu Leu Ala Gly
785                 790                 795                 800

His Cys Thr Ala Arg Glu Pro Tyr Gln Arg Pro Asp Met Gly His Ala
                805                 810                 815

Val Asn Val Leu Val Pro Leu Val Glu Gln Trp Lys Pro Thr Ser His
            820                 825                 830

Asp Glu Glu Glu Glu Asp Gly Ser Gly Gly Asp Leu His Met Ser Leu
```

```
          835                    840                    845

Pro Gln Ala Leu Arg Arg Trp Gln Ala Asn Glu Gly Thr Ser Ser Ile
    850                    855                    860

Phe Asn Asp Ile Ser Ile Ser Gln Thr Gln Ser Ser Ile Ser Ser Lys
865                    870                    875                    880

Pro Ala Gly Phe Ala Asp Ser Phe Asp Ser Met Asp Cys Arg
               885                    890
```

```
<210>      1119
<211>      894
<212>      PRT
<213>      Glycine max

<223>      Seq ID: rhg4_peking_amplicon

<400>      1119

Met Ser Asn Phe Leu Lys Ser Leu Thr Pro Pro Pro Ser Gly Trp Ser
1               5                   10                  15

Glu Thr Thr Pro Phe Cys Gln Trp Lys Gly Ile Gln Cys Asp Ser Ser
            20                  25                  30

Ser His Val Thr Ser Ile Ser Leu Ala Ser Gln Ser Leu Thr Gly Thr
        35                  40                  45

Leu Pro Ser Asp Leu Asn Ser Leu Ser Gln Leu Arg Thr Leu Ser Leu
    50                  55                  60

Gln Asp Asn Ser Leu Thr Gly Thr Leu Pro Ser Leu Ser Asn Leu Ser
65                  70                  75                  80

Phe Leu Gln Thr Val Tyr Phe Asn Arg Asn Asn Phe Ser Ser Val Ser
            85                  90                  95

Pro Thr Ala Phe Ala Ser Leu Thr Ser Leu Gln Thr Leu Ser Leu Gly
            100                 105                 110

Ser Asn Pro Ala Leu Gln Pro Trp Ser Phe Pro Thr Asp Leu Thr Ser
        115                 120                 125

Ser Ser Asn Ile Asp Leu Asp Leu Ala Thr Val Ser Leu Thr Gly
    130                 135                 140

Pro Leu Pro Asp Ile Phe Asp Lys Phe Pro Ser Leu Gln His Leu Arg
145                 150                 155                 160

Leu Ser Tyr Asn Asn Leu Thr Gly Asn Leu Pro Ser Ser Phe Ser Ala
            165                 170                 175

Ala Asn Asn Leu Glu Thr Leu Trp Leu Asn Asn Gln Ala Ala Gly Leu
        180                 185                 190

Ser Gly Thr Leu Leu Val Leu Ser Asn Met Ser Ala Leu Asn Gln Ser
```

```
         195                    200                    205

Trp Leu Asn Lys Asn Gln Phe Thr Gly Ser Ile Pro Asp Leu Ser Gln
    210                   215                   220

Cys Thr Ala Leu Ser Asp Leu Gln Leu Arg Asp Asn Gln Leu Thr Gly
225                   230                   235                   240

Val Val Pro Ala Ser Leu Thr Ser Leu Pro Ser Leu Lys Lys Val Ser
              245                   250                   255

Leu Asp Asn Asn Glu Leu Gln Gly Pro Val Pro Val Phe Gly Lys Gly
              260                   265                   270

Val Asn Val Thr Leu Asp Gly Ile Asn Ser Phe Cys Leu Asp Thr Pro
              275                   280                   285

Gly Asn Cys Asp Pro Arg Val Met Val Leu Leu Gln Ile Ala Glu Ala
    290                   295                   300

Phe Gly Tyr Pro Ile Arg Leu Ala Glu Ser Trp Lys Gly Asn Asp Pro
305                   310                   315                   320

Cys Asp Gly Trp Asn Tyr Val Val Cys Ala Ala Gly Lys Ile Ile Thr
              325                   330                   335

Val Asn Phe Glu Lys Gln Gly Leu Gln Gly Thr Ile Ser Pro Ala Phe
              340                   345                   350

Ala Asn Leu Thr Asp Leu Arg Thr Leu Phe Leu Asn Gly Asn Asn Leu
              355                   360                   365

Ile Gly Ser Ile Pro Asp Ser Leu Ile Thr Leu Pro Gln Leu Gln Thr
    370                   375                   380

Leu Asp Val Ser Asp Asn Asn Leu Ser Gly Leu Val Pro Lys Phe Pro
385                   390                   395                   400

Pro Lys Val Lys Leu Val Thr Ala Gly Asn Ala Leu Leu Gly Lys Pro
              405                   410                   415

Leu Ser Pro Gly Gly Gly Pro Ser Gly Thr Thr Pro Ser Gly Ser Ser
              420                   425                   430

Thr Gly Gly Ser Gly Gly Glu Ser Ser Lys Gly Asn Ser Ser Val Ser
              435                   440                   445

Pro Gly Trp Ile Ala Gly Ile Val Val Ile Val Leu Phe Phe Ile Ala
    450                   455                   460

Val Val Leu Phe Val Ser Trp Lys Cys Phe Val Asn Lys Leu Gln Gly
465                   470                   475                   480

Lys Phe Ser Arg Val Lys Gly His Glu Asn Gly Lys Gly Gly Phe Lys
              485                   490                   495

Leu Asp Ala Val His Val Ser Asn Gly Tyr Gly Gly Val Pro Val Glu
              500                   505                   510
```

```
Leu Gln Ser Gln Ser Ser Gly Asp Arg Ser Asp Leu His Ala Leu Asp
        515              520              525
Gly Pro Thr Phe Ser Ile Gln Val Leu Arg Gln Val Thr Asn Asn Phe
    530              535              540
Ser Glu Glu Asn Ile Leu Gly Arg Gly Gly Phe Gly Val Val Tyr Lys
545              550              555              560
Gly Val Leu His Asp Gly Thr Lys Ile Ala Val Lys Arg Met Glu Ser
            565              570              575
Val Ala Met Gly Asn Lys Gly Gln Lys Glu Phe Glu Ala Glu Ile Ala
        580              585              590
Leu Leu Ser Lys Val Arg His Arg His Leu Val Ala Leu Leu Gly Tyr
        595              600              605
Cys Ile Asn Gly Asn Glu Arg Leu Leu Val Tyr Glu Tyr Met Pro Gln
    610              615              620
Gly Thr Leu Thr Gln His Leu Phe Glu Trp Gln Glu His Gly Tyr Ala
625              630              635              640
Pro Leu Thr Trp Lys Gln Arg Val Val Ile Ala Leu Asp Val Ala Arg
            645              650              655
Gly Val Glu Tyr Leu His Ser Leu Ala Gln Gln Ser Phe Ile His Arg
            660              665              670
Asp Leu Lys Pro Ser Asn Ile Leu Leu Gly Asp Asp Met Arg Ala Lys
        675              680              685
Val Ala Asp Phe Gly Leu Val Lys Asn Ala Pro Asp Gly Lys Tyr Ser
    690              695              700
Val Glu Thr Arg Leu Ala Gly Thr Phe Gly Tyr Leu Ala Pro Glu Tyr
705              710              715              720
Ala Ala Thr Gly Arg Val Thr Thr Lys Val Asp Val Tyr Ala Phe Gly
            725              730              735
Val Val Leu Met Glu Leu Ile Thr Gly Arg Lys Ala Leu Asp Asp Thr
            740              745              750
Val Pro Asp Glu Arg Ser His Leu Val Thr Trp Phe Arg Arg Val Leu
    755              760              765
Ile Asn Lys Glu Asn Ile Pro Lys Ala Ile Asp Gln Ile Leu Asn Pro
    770              775              780
Asp Glu Glu Thr Met Gly Ser Ile Tyr Thr Val Ala Glu Leu Ala Gly
785              790              795              800
His Cys Thr Ala Arg Glu Pro Tyr Gln Arg Pro Asp Met Gly His Ala
            805              810              815
```

```
Val Asn Val Leu Val Pro Leu Val Glu Gln Trp Lys Pro Thr Ser His
            820                 825                 830

Asp Glu Glu Glu Asp Gly Ser Gly Gly Asp Leu His Met Ser Leu
        835                 840                 845

Pro Gln Ala Leu Arg Arg Trp Gln Ala Asn Glu Gly Thr Ser Ser Ile
    850                 855                 860

Phe Asn Asp Ile Ser Ile Ser Gln Thr Gln Ser Ser Ile Ser Ser Lys
865                 870                 875                 880

Pro Ala Gly Phe Ala Asp Ser Phe Asp Ser Met Asp Cys Arg
                885                 890
```

<210> 1120

<211> 23

<212> PRT

<213> Artificial

<223>   Seq ID: consensusLRR

<400> 1120

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Leu Phe Ser Asn Leu Pro Asn Leu Glu Glu Leu Asp Leu Ser Asn Asn
1               5                 10                  15

Leu Thr Ser Leu Pro Pro Gly
            20
```

<210> 1121

<211> 289

<212> PRT

<213> Artifical

<223>   Seq ID: rhg1LRR

<400> 1121

```
Thr Leu Gly Leu Leu Pro Gly Leu Arg Lys Leu Ser Leu His Asp Asn
1               5                 10                  15

Gln Ile Gly Gly Ser Ile Pro Ser Ser Leu Gly Phe Cys Pro Asn Leu
            20                  25                  30

Arg Gly Val Gln Leu Phe Asn Asn Arg Leu Thr Gly Ser Ile Pro Leu
        35                  40                  45
```

1220

```
Leu Ala Asn Ser Thr Leu Leu Gln Ser Leu Asp Leu Ser Asn Asn Leu
    50                      55                  60

Leu Thr Gly Ala Ile Pro Tyr Ser Leu Thr His Ser Phe Lys Leu Tyr
65                  70                  75                  80

Trp Leu Asn Leu Ser Phe Asn Ser Phe Ser Gly Pro Leu Pro Ala Ser
                85                  90                  95

Trp Gly Gly Asn Ser Lys Ser Leu Thr Phe Leu Ser Leu Gln Asn Asn
            100                 105                 110

Asn Leu Ser Gly Ser Leu Pro Asn Ser Leu Gly Ser Leu Arg Arg Leu
        115                 120                 125

Gln Asn Leu Ile Leu Asp His Asn Phe Phe Thr Gly Asp Val Pro Ala
    130                 135                 140

Ser Ile Gly Thr Leu Ser Glu Leu Asn Glu Leu Ser Leu Ser His Asn
145                 150                 155                 160

Lys Phe Ser Gly Ala Ile Pro Asn Glu Thr Leu Ser Asn Leu Ser Arg
            165                 170                 175

Leu Lys Thr Leu Asp Ile Ser Asn Asn Ala Leu Asn Gly Asn Leu Pro
            180                 185                 190

Ala Ser Leu Gly Arg Leu Arg Ser Leu Thr Leu Leu Asn Ala Glu Asn
        195                 200                 205

Asn Leu Leu Asp Asn Gln Ile Pro Gln Ser Ile Ala Asn Ile Ser Asn
    210                 215                 220

Leu Ser Val Leu Ile Leu Ser Arg Asn Gln Phe Ser Gly His Ile Pro
225                 230                 235                 240

Ser Ser Phe Asp Ser Gln Arg Ser Leu Arg Gln Leu Asp Leu Ser Leu
            245                 250                 255

Asn Asn Phe Ser Gly Glu Ile Pro Val Leu Leu Ala Lys Lys Phe Asn
            260                 265                 270

Ser Leu Asn Leu Phe Asn Val Ser Asn Ser Leu Ser Gly Ser Val Pro
        275                 280                 285

Pro


<210>   1122

<211>   281

<212>   PRT

<213>   Artificial
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1221

<223>   Seq ID: Rhg4LRR

<400>   1122

His Val Thr Ser Ile Ser Leu Ala Ser His Ser Leu Thr Gly Thr Leu
1   5   10   15

Pro Ser Asp Leu Asn Ser Leu Ser Gln Leu Arg Thr Leu Ser Leu Gln
            20   25   30

Asp Asn Ser Leu Gly Thr Leu Pro Ser Leu Ser Asn Leu Ser Phe Leu
        35   40   45

Gln Thr Val Tyr Leu Asn Arg Asn Asn Phe Ser Ser Val Pro Thr Ala
    50   55   60

Phe Ala Ser Leu Thr Ser Leu Gln Thr Leu Ser Leu Gly Ser Asn Pro
65   70   75   80

Ala Leu Gln Pro Trp Ser Phe Pro Thr Asp Leu Thr Ser Ser Ser Asn
            85   90   95

Leu Ile Asp Leu Asp Leu Ala Thr Val Ser Leu Thr Gly Pro Leu Pro
            100   105   110

Asp Ile Phe Asp Lys Phe Pro Ser Leu Gln His Leu Arg Leu Ser Tyr
        115   120   125

Asn Asn Leu Thr Gly Asn Leu Pro Ser Ser Phe Ser Ala Ala Asn Asn
    130   135   140

Leu Glu Thr Leu Trp Leu Asn Asn Gln Ala Ala Gly Leu Ser Gly Thr
145   150   155   160

Leu Leu Leu Ser Asn Met Ser Ala Leu Ser Asp Leu Gln Leu Arg Asp
            165   170   175

Asn Gln Leu Thr Gly Val Val Pro Ala Ser Leu Thr Ser Leu Pro Ser
            180   185   190

Leu Lys Lys Val Ser Leu Asp Asn Asn Glu Leu Gln Gly Pro Val Pro
        195   200   205

Val Phe Gly Lys Gly Val Asn Lys Ile Ile Thr Val Asn Phe Glu Lys
    210   215   220

Gln Gly Leu Gln Gly Thr Ile Ser Pro Ala Phe Ala Asn Leu Thr Asp
225   230   235   240

Leu Arg Thr Leu Phe Leu Asn Gly Asn Asn Leu Ile Gly Ser Ile Pro
            245   250   255

Asp Ser Leu Ser Ile Thr Leu Pro Gln Leu Gln Thr Leu Asp Val Ser Asp
        260   265   270

Asn Asn Leu Ser Gly Leu Val Pro Lys
    275   280

```
<210>  1123

<211>  27

<212>  DNA

<213>  Glycine max


<223>      Seq ID: 240017_region_G3_forward_1_b

<400>  1123

gttgtatgga tggtaaaaat tcaaaac                                        27
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